

QY 301 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 360
|||||
Db 7573 GCAATGAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTTCAGAAAGTTTGAAGCACCATGGT 7632
QY 361 GTGTCATGCTCACTTTTGTGAAAGCTGCTGCTCAGAGTCTATCAACATTTGAATATCAG 420
|||||
Db 7633 GTGTCATGCTCACTTTTGTGAAAGCTGCTGCTCAGAGTCTATCAACATTTGAATATCAG 7692
QY 421 TTGACAGAAATGGTGCCATGGCGGCTAACATCCCTGCTTTGATTCCTCTGATAAGCTGTT 480
|||||
Db 7693 TTGACAGAAATGGTGCCATGGCGGCTAACATCCCTGCTTTGATTCCTCTGATAAGCTGTT 7752
QY 481 CTGGTGGCAGTAACATGCCAAC 501
|||||
Db 7753 CTGGTGGCAGTAACATGCCAAC 7773

Search completed: April 4, 2003, 06:43:23
Job time : 71.6923 secs

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 566.323 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526C-1_COPY_7250_7750
Perfect score: 501
Sequence: 1 ttacagggcagtgctttg.....tggtggcagtaacatgcaac 501

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST.*
- 1: en_estba.*
- 2: en_esthum.*
- 3: en_estin.*
- 4: en_estnu.*
- 5: en_estov.*
- 6: en_estpl.*
- 7: en_estro.*
- 8: em_hic.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: gb_gss.*
- 18: em_gss_hum.*
- 19: em_gss_inv.*
- 20: em_gss_pln.*
- 21: em_gss_vrt.*
- 22: em_gss_fun.*
- 23: em_gss_man.*
- 24: em_gss_mus.*
- 25: em_gss_other.*
- 26: em_gss_pro.*
- 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	391	78.0	429	14	N46182
2	230.2	45.9	653	10	AW918387
3	197.4	39.4	3065	11	AK019548
c 4	196.2	39.2	582	10	BE110717
5	193.2	38.6	699	9	AA124253
6	186.8	37.3	832	13	BI662985

c 7	167.6	33.5	324	12	BG002542
c 8	153.4	30.6	902	9	AI323676
c 9	148.6	29.7	654	9	AI323285
c 10	141.4	28.2	289	9	AA964962
c 11	140.2	28.0	408	12	BF411653
c 12	128.6	25.7	257	10	AW915133
c 13	120.2	24.0	246	9	AA850189
c 14	109	21.8	483	17	AA310595
c 15	95.2	19.0	634	17	BH290554
c 16	84.2	16.8	753	9	AJ456659
c 17	61.2	12.2	166	10	BE183556
c 18	61.2	12.2	765	13	BI078318
c 19	58.6	11.7	658	13	BM426183
c 20	57	11.4	238	12	BF740733
c 21	43.8	8.7	563	14	BQ394625
c 22	43.6	8.7	240	9	AI441280
c 23	43.2	8.6	647	17	AQ428886
c 24	43.2	8.6	668	13	BM159718
c 25	43.2	8.6	704	13	BM162478
c 26	42	8.4	755	13	BI908180
c 27	41.8	8.3	646	12	BQ331196
c 28	41.6	8.3	987	17	CNS014PQ
c 29	40.8	8.1	523	13	BJ344889
c 30	40.6	8.1	1101	17	CNS001QW
c 31	40.4	8.1	271	10	BB578327
c 32	40.4	8.1	491	9	AI953982
c 33	40.2	8.0	710	17	AQ450260
c 34	40.2	8.0	942	17	CNS00C8A
c 35	40.2	8.0	1023	17	CNS00LA0
c 36	40	8.0	454	9	AI300555
c 37	39.8	7.9	234	9	AL118620
c 38	39.8	7.9	1101	17	CNS017KX
c 39	39.6	7.9	648	17	AJ186649
c 40	39.6	7.9	761	12	BG219214
c 41	39.4	7.9	784	10	BE537207
c 42	39.2	7.8	428	13	BI270529
c 43	39.2	7.8	1100	17	CNS00FSE
c 44	39	7.8	356	9	AL501209
c 45	39	7.8	386	17	AQ953885

ALIGNMENTS

RESULT 1
LOCUS N46182
DEFINITION YV38a07.r1 Soares melanocyte 2NdhM Homo sapiens CDNA clone
IMAGE:273492.5, mRNA linear EST 14-FEB-1996
ACCESSION N46182
VERSION N46182.1 GI:1187348
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 430.

FEATURES	source	Location/Qualifiers
		1. .429
		/organism="Homo sapiens"
		/db_xref="GDB:3883134"
		/db_xref="taxon:9606"
		/clone="IMAGE:273492"
		/clone_lib="Soares melanocyte 2NbHM"
		/sex="Male"
		/tissue_type="melanocyte"
		/lab_host="DH10B (ampicillin resistant)"
		/note="Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5'
		TGTTACCAATCTGAAGTGGAGCGCGCCGAGTTTTTTTTTTTTTTT 3'],
		double-stranded cDNA was size selected, ligated to Eco RI
		adapters (Pharmacia), digested with Not I and cloned into
		the Not I and Eco RI sites of a modified pT73 vector
		(Pharmacia). Library constructed by Bento Soares and
		M.Fatima Bonaldo. RNA from normal foreskin melanocytes
		(FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT	114 a	87 c 91 g 136 t 1 others
ORIGIN		
		Query Match 78.0%; Score 391; DB 14; Length 429;
		Best Local Similarity 99.3%; Pred. No. 3.3e-65;
		Matches 413; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY	88	A A C T C T A T T A T G G A A C C C A A T G G A C A T A T G G T T G A A C T C A C A C - T T T T T T T T T T T T T 146
Db	2	A A N T C T A T T A T G G A A C C C A A T G G A C A T A T G G T T G A A C T C A C A C T T T T T T T T T T T 61
QY	147	T G T T C C T G T A T C T C A T T G G G T T G C A C A A T A T T C A T C A A G T A A T C A T G C C A G C 206
Db	62	T G T T C C T G T A T C T C A T T G G G T T G C A C A A T A T T C A T C A A G T A A T C A T G C C A G C 121
QY	207	A T T A T T G A T C A A A T C A A A A G G T T A A T G C A C A T C C T C A T T C A C T A A G C C A T G C C A C 266
Db	122	A T T A T T G A T C A A A A T C A A A A G G T T A A T G C A C A T C C T C A T T C A C T A A G C C A T G C C A C 181
QY	267	G G A G A C T G G T T T C C G G T G A C A C A T C C A T T C G T G C A A T G A G T G T C C A G A G T T A T A G T 326
Db	182	G G A G A C T G G T T T C C G G T G A C A C A T C C A T T G T G G C A T G A G T G T C C A G A G T T A T A G T 241
QY	327	G C C A A G T T T T T C A A A A G T T T A A G C A C C A T G T G T G T C A T G C T A C T T T T G T G A A A G C T 386
Db	242	G C C A A G T T T T T C A A A A G T T T A A G C A C C A T G T G T G T C A T G C T A C T T T T G T G A A A G C T 301
QY	387	G C T C T C T C A G A G T C T A T C A C A T T C A A T A T C A G T T C A G A G A T G T G C C A T G C G T G G C T 446
Db	302	G C T C T C T C A G A G T C T A T C A C A T T C A A T A T C A G T T C A G A G A T G T G C C A T G C G T G G C T 361
QY	447	- A A C A T C C T G C T T T G A T T C C C T G T A T A A G C T G T T C T G T G G C A G T A A C A T G C A A C 501
Db	362	A A A C A T C C T G C T T T G A T T C C C T C T G A T A A G C T G T T C T G T G G C A G T A A C A T G C A A C 417
RESULT 2		
AW918387		653 bp mRNA linear EST 25-MAY-2000
LOCUS		EST349691 Rat gene index, normalized rat, norvegicus, Bento Soares
DEFINITION		Rattus norvegicus cDNA clone RGI858 5' end, mRNA sequence.
ACCESSION		AW918387
VERSION		AW918387.1 GI:8084163
KEYWORDS		EST.
SOURCE		Norway rat.
ORGANISM		Rattus norvegicus
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
		Rattus.
REFERENCE		1 (bases 1 to 553)
AUTHORS		Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J.,
		Kerlavage,A.R. and Adams,M.D.
TITLE		Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat

AK019548
 VERSION AK019548.1 GI:12859824
 KEYWORDS HPC: CAP trapper.
 SOURCE Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_11b:RIKEN full-length enriched mouse cDNA library
 Cloned: 4921533G24.
 Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 REFERENCE Carninci, P., and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 95279253
 PUBMED 10349636
 2
 REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 3
 REFERENCE Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Inoue, K., Inoue, K., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 4
 REFERENCE Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L., Staab, P., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, S., Blake, J., Brownstein, M. J., Bult, C., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., H., Kohtsuki, S., and Hayashizaki, Y.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 5
 REFERENCE (bases 1 to 3065)
 AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I.,

Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTITTTTIVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTAATTAATTAATCCGCCGCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="FANTOM:DB:4921533G24"
 /db_xref="MGD:MGI:1912764"
 /db_xref="taxon:10090"
 /clone="4921533G24"
 /sex="male"
 /tissue_type="testis"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="adult"
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 /gene="Abca1"
 misc_feature 1..3065
 /gene="Abca1"
 /note="ATP-binding cassette, sub-family A (ABCI), member 1"
 data source:MGD, source key:MGI:99607, evidence:ISS
 /db_xref="MGD:MGI:99607"
 BASE COUNT 930 a 581 c 567 g 987 t
 ORIGIN
 Query Match 39.4%; Score 197.4; DB 11; Length 3065;
 Best Local Similarity 72.6%; Pred. No. 1.5e-28;
 Matches 368; Conservative 0; Mismatches 121; Indels 18; Gaps 8;
 QY 1 TTACAGGGGAGTGCCTTTTACCTATGCTTGTATGGCTCTCAAGTGAA--GACTTG 58
 DB 84 TTACAGGGGAGTGCCTTTTACCTATGCTTGTATGGCTCTCTAGTGAATGACTTG 143
 QY 59 AATTAGCTTTTACC-TATACCTATGTGAACCTATATGGAACCAATGGACATATG 117
 DB 144 AGTTAGTTCATTACCTTATACAGATGTGAACCTCTGGTGGNACCAAGACTCTGG 203
 QY 118 GGTTCAGCTCAGACATTTTTCCTTCCTGCTGATTCATTCATTCGGTTCGCAAC 177
 DB 204 GTTTGGA-----TTCATACCTTTTTCCTGCTGATTCCTACTAGGATTCGCAAC 254
 QY 178 AATAATTCATCAAGTAATCATGCCGCGATTATGATCAAAATCAAAAGTAAATGCACA 237
 DB 255 AACAGTCTCAATAGTCAATGCGCAGTGTATATCAAGTCAAGGACACACATCTCG 314
 QY 238 TCC-TCAATCAAGCCATGCCATGCCAGGAGACTGGTTTCCCGTGACACATCCATT 296
 DB 315 TCCATTAAAGCCATTAAAGCCATGCTGAACCAAAACAGGTTTCCCGTGACACATCCATT 374

QY 297 GCTGGCAATGAGTGTGCCAGAGTTATTAGGCCCAAGTTTTTCAGAAAGTTTGAAGCACCA 356
 Db 375 GCTGGCAATGAGTGTGCCAGAGTTACTAGTGGCAAGTTGCTCAGAAAGTCTGAAGCA-CT 433
 QY 357 TGGTGTGTCATGCTCAGCTTTTGTGAAGCTGCTGCTGCTCAGAGTCTATCAACATTTGAATA 416
 Db 434 GAGTGTGTCACAAACACTTTTGTGAAGCCGCCCTACTGTCGGT-TGACATCATTAATA 492
 QY 417 TCAGTTGAC-AGAATGGTGCATGCGTGGCTAAACATCCTGCTTTGATTCCCTC--TGATA 473
 Db 493 TCAGTGCACAAACGCTGGCCACATGACTGAATCCCAATTTCTCTCTCTTTGATG 552
 QY 474 AGCTGTTCTGGTGGCCAGTAACATGCAA 500
 Db 553 AGCTGCTGTTGCTGCTCTGTACAA 579

RESULT 4
 LOCUS BEL10717/c
 DEFINITION UI-R-BJ1-avd-f-06-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
 ACCESSION BEL10717
 VERSION 1
 KEYWORDS EST.
 SOURCE Rattus.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

1 (bases 1 to 582)
 REFERENCE 1 (bases 1 to 582)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized AV canal at 15 dpc library cDNA Library Preparation:
 M.B. Soares Lab Clone Distribution: clones will be available
 through Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=Yes.

FEATURES
 Source Location/Qualifiers
 1..582
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BJ1-avd-f-06-0-UI"
 /clone_lib="UI-R-BJ1"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1
 library is a subtracted library derived from the following
 tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
 canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,
 AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.
 For a detailed description of the library from which this
 clone was derived, please visit our web site at
 ratseq.eng.uiowa.edu. The subtraction has been previously
 described in (Bonaldo, Lennon and Soares, Genome Research
 6:791-806, 1996)
 TAG_LIB=UI-R-BJ1

BASE COUNT 157 a 129 c 123 g 173 t
 ORIGIN
 Query Match 39.2%; Score 196.2; DB 10; Length 582;
 Best Local Similarity 76.9%; Pred. No. 4.6e-28;
 Matches 336; Conservative 0; Mismatches 78; Indels 23; Gaps 7;
 QY 1 TTACAGGGGCGAGTGGCTTTGTAGCCTATGCTCTTGTATGCTCTCAAGTGAA--GACTTG 58
 Db 434 TTACAGGGGCGAGTGGCTTTGTAGCCTATGCTCTTGTATGCTCTCAAGTGAA--GACTTG 58
 QY 59 AATTTAGTTTTTTA-CCTATACCTATGTGAACCTCTATTATGGAACCAATGGACATATG 117
 Db 374 AAGTTAGTTTCTATTCTATGAGATGTGAACCTCTGTTGGAACCAAGAGACTCTGG 315
 QY 118 GCTTTGAACCTACACTTTTTTTTTTTTTTTTTTGTCTGTATCTCTCATTTGGGGTTGCAAC 177
 Db 314 GTTTGGA-----TTCATCTGTTTGTCTGTATCTCTCACTGGGANTTGAAC 266
 QY 178 AATAATTCATCAAGTAATCATGCGCAGCGATTATTGATCAAAATCAAAAGTAATGCACA 237
 Db 265 AACATCCGTCAGTAGTCATGCGCAGTGATAT-----CAACGTCGAAGGCATGTACA 212
 QY 238 TCCTCATCTACTAAGCCATGCCATGCCAGGAGACTGTTTCCCGGTGACACATCCATTG 297
 Db 211 TCCTCATCTACTAAGCCATG-CTGACCCACAAACCTGTTTCCCGGTGACACATCCATTG 153
 QY 298 CTGGCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTTTCAGAAAGTTTGAAGCCCAT 357
 Db 152 CTGGCAATGAGTGTGCCAGAGTTATTAGTCCCAAGTTTCTCAGAAAGTCTCAAGCACATA- 94
 QY 358 GGTGTGTCATGCTACTCTTTTGTGAAGCTGCTCTCTCAGAGTCTATCAACATTTGAATAT 417
 Db 93 AGTATGTCACAAACACTTTTGTGAACCCGCGCTCTCTCTGT-TGACATCATTAATAT 35
 QY 418 CAGTTGACAGATGGTG 434
 Db 34 CAGGTGACAAACCGGTG 18

RESULT 5
 LOCUS AA124253
 DEFINITION mq2ig08.r1 Barstead MRLB1 Mus musculus cDNA clone IMAGE:579422 5'
 similar to gb:X75926 M.musculus abcl mRNA (MOUSE);, mRNA sequence.
 AA124253
 ACCESSION AA124253
 VERSION AA124253.1 GI:1682819
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 699)
 REFERENCE 1 (bases 1 to 699)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMNI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMNI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:354070
 Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 506.
Location/Qualifiers
1. .699
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:579422"
/clone_lib="Barstead MFLRB1"
/sex="mixed"
/tissue_type="kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
/note="Vector: p7n3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5', TGTACGAATCGAATGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [CATGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead."

BASE COUNT 201 a 150 c 156 g 192 t
ORIGIN

Query Match 38.6%; Score 193.2; DB 9; Length 699;
Best Local Similarity 72.8%; Pred. No. 1.6e-27;
Matches 361; Conservative 0; Mismatches 118; Indels 17; Gaps 8;

QY 1 TTACAGGGCAGTCCCTTTAGCCATGCTGTATGGCTCTCAAGTGA--GACTTG 58
Db 215 TTACAGGGCAGTCCCTTTAGCCATGCTGTATGGCTCTCTAGTGAATGACTTG 274

QY 59 AATTAGTTTTTACC-TATACCTATGTGAACCTCTATTATGAACCAATGGACATATG 117
Db 275 AAGTTAGTTTACCTATACAGATGTGAACCTCTGTGGTGGCAACACGACACTCTGG 334

QY 118 GGTGTAACACACATTTTTTTTTTTTTCCTCTGTGTTCTCATTTGGGGTTGCAAC 177
Db 335 GTTTGGA-----TTCATACCTTTTTTTTTCCTCTGTGTTCTCATTTGGGGTTGCAAC 385

QY 178 AATAAATTCATCAAGTATGATGCGCCAGTATTATGATCAAAATCAAAAGTTGAAGCACA 237
Db 386 AACAGTCTATCAATAGTATGCGCCAGTATATCAAAAGTCAAAAGCAGACATCTCTCG 445

QY 238 TCC-TCAATTCATTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATT 296
Db 446 TCCATTAAAGCCATTAAAGCCATGCTGAACCAACAAACAGGTTTCCCGGTGACACATCCATT 505

QY 297 GCTGGCAATGAGTGTGCGAGAGTATTAGTGCACAAAGTTTTTCAGAAAGTTGAAGCACA 356
Db 506 CTGGCAATGAGTGTGCGAGAGTATTAGTGCACAAAGTTGCTCAGAAAGTCTGAAGCA-CT 564

QY 357 TGGTGTGTCATGCTCACTTTTGTGAAGAGTGTCTGCTCAGAGTCTATCAACATTTGAATA 416
Db 565 GAGTGTGTCACCAACACTTTTGTGAAGAGTGTCTGCTCAGAGTCTATCAACATTTGAATA 623

QY 417 TCAGTTGAC-AGATGTTGCGCATGCGTGAACATCTCTGTTGAT-TCCTCTGTATA 474
Db 624 TCAGTTGAC-AGATGTTGCGCATGCGTGAACATCTCTGTTGAT-TCCTCTGTATA 683

QY 475 GCTGTTCTGTTGGCAG 490
Db 684 GCTGTTCTGTTGGCAG 699

RESULT 6
BI662985 832 bp mRNA linear EST 12-SEP-2001
LOCUS 603286357F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5320238 5',
DEFINITION mRNA sequence.
ACCESSION BI662985
VERSION BI662985.1 GI:15577218
KEYWORDS EST.
SOURCE house mouse.

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 832)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1812 row: b column: 15
High quality sequence stop: 809.
FEATURES
Location/Qualifiers
1. .832
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5320238"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies, Inc. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 225 a 185 c 184 g 238 t
ORIGIN

Query Match 37.3%; Score 186.8; DB 13; Length 832;
Best Local Similarity 74.4%; Pred. No. 2.5e-26;
Matches 345; Conservative 0; Mismatches 102; Indels 17; Gaps 8;

QY 1 TTACAGGGCAGTCCCTTTAGCCATGCTGTATGGCTCTCAAGTGA--GACTTG 58
Db 263 TTACAGGGCAGTCCCTTTAGCCATGCTGTATGGCTCTCTAGTGAATGACTTG 322

QY 59 AATTAGTTTTTACC-TATACCTATGTGAACCTCTATTATGAACCAATGGACATATG 117
Db 323 AAGTTAGTTTACCTATACAGATGTGAACCTCTGTGGTGGCAACAGCAGAC-TCTG 381

QY 118 GGTGTAACACACATTTTTTTTTTTTTCCTCTGTGTTCTCATTTGGGGTTGCAAC 177
Db 382 GGTGTAACACATTTTTTTTTTTTTCCTCTGTGTTCTCATTTGGGGTTGCAAC 432

QY 178 AATAAATTCATCAAGTATGATGCGCCAGTATTATGATCAAAATCAAAAGTTGAAGCACA 237
Db 433 AACAGTCTATCAATAGTATGCGCCAGTATATCAAAAGTCAAAAGCAGACATCTCTCG 492

QY 238 TCC-TCAATTCATTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGACACATCCATT 296
Db 493 TCATTAAAGCCATTAAAGCCATGCTGAACCAACAAACAGGTTTCCCGGTGACACATCCATT 552

QY 297 GCTGGCAATGAGTGTGCGAGAGTATTAGTGCACAAAGTTTTTCAGAAAGTTGAAGCACA 356
Db 553 GCTGGCAATGAGTGTGCGAGAGTATTAGTGCACAAAGTTGCTCAGAAAGTCTGAAGCA-CT 611

QY 357 TGGTGTGTCATGCTCACTTTTGTGAAGAGTGTCTCTGCTCAGAGTCTATCAACATTTGAATA 416
Db 612 GAGTGTGTCACAAACACTTTTGTGAAGAGTGTCTCTGCTCAGAGTCTATCAACATTTGAATA 670

QY 417 TCAGTTGAC-AGATGTTGCGCATGCGTGAACATCTCTGTTGAT-TCCTCTGTATA 459
Db 671 TCAGTTGAC-AGATGTTGCGCATGCGTGAACATCTCTGTTGAT-TCCTCTGTATA 714

Db 648 ACAAGTCTATCAAAATAGTCATGCCAGTGATCAAAAGTCAAAAGGCACACATCTTGG 589
 QY 236 CATCCCTCAITCACTAAGCCATGCGCATGCCAGAGACTGGTTCCGGGTGACACATCCAT 295
 Db 588 TCATTAGCCATTAAGCCATGCTGACCCACANACAGTTTCCCGNGTGACATCCAT 529
 QY 296 TGTGCAATAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTTTCAGAAAGTTTGAAGCAC 355
 Db 528 TGTGCAATAGTGTGCCAGAGTTATTAGTGCCAAAGTTTTCAGANAGTCTGAAGCA-C 470
 QY 356 ATGGTGTGTCATGCTCACITTTTGTGAAGTCTGCTGCTCAGAGTCTATCAACATTTGAT 415
 Db 469 TGAGTGTGTCACAAACACITTTTGTGAAGCCGCCCTACTGTGGT-TGACATCAITTAAT 411
 QY 416 ATCAGTTGAC-AGAATGGTGCCATGCTGCTAACATCCTGTTGATCCCTC--TGAT 472
 Db 410 ATCAGGTGACAAACAGGTGCCCATGTGACTAAATCCCATTTTCTCTCTCTTTGAT 351
 QY 473 AAGCTGTTCTGGTGGCAGTAAACATGCAA 500
 Db 350 GAGCTGCTGTTGGTGTCTTGTCTTGTACAA 323

RESULT 9
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 LOCUS mq21g08.y1 Barstead MPLR1 Mus musculus cdna clone IMAGE:579422 5'
 DEFINITION similar to gb:X75926 M.musculus abcl mRNA (MOUSE);, mRNA sequence.
 ACCESSION AI323285
 VERSION AI323285.1 GI:4057714
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 654)
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, I., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 CONTACT: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:354070

FEATURES
 source
 1..654
 /organism="Mus musculus"
 /strain="BAUB/c"
 /db_xref="taxon:10090"
 /clone="IMAGE:579422"
 /clone_lib="Barstead MPLR1"
 /sex="mixed"
 /tissue_type="Kidney"
 /dev_stage="6 weeks"
 /lab_host="DH108"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cdna
 was primed with a Not I - oligo(dT) primer [5']

TGTTACGAATCTAAGTGGGAGCGCCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 [CATGGATTGGTACC], digested with Not I and cloned into the
 Not I and Eco RI sites of the modified pT73 vector.
 Library constructed by Bob Barstead.
 BASE COUNT 190 a 144 c 146 g 173 t 1 others
 ORIGIN

Query Match 29.7%; Score 148.6; DB 9; Length 654;
 Best Local Similarity 74.2%; Pred. No. 5.3e-19;
 Matches 259; Conservative 0; Mismatches 74; Indels 16; Gaps 5;
 QY 1 TTACAGGGCAGTGGCTTTGTAGCCTATGTCTGTATGGCTCTCAAGTGAA--GACTTG 58
 Db 221 TTACAGGGCAGTGGCTTTGTAGCCTATGTCTGTATGGCTCTAGTGAATAACTG 280
 QY 59 AATTAGTTTATAC--TATACCTATGTCAAACTCTATTATGGAACCCAAATGGACATATG 117
 Db 281 AAGTTAGTTCATTACCTTATACAGATGAAACTCTGGTGTGGAACCAAGCAGACTCGG 340
 QY 118 GGTGTAACACACATTTTTTTTTTTTTTTTGTTCCTGTATTCCTCATTTGGGGTTCGAAC 177
 Db 341 GTTTGGA-----TTCATACTTTTTTTTGTCTGTATTCCTCACTAGGATTGCAAC 391
 QY 178 AATAATTCATCAAGTAATCATGGCCAGCATTTATGA--TCAAAATCAAAAGGTATATGA 235
 Db 392 AACAGTCTAATCAATAGTATGCGCAGTGATATCAAAAGTCAAGGCACACCACCTCT 451
 QY 236 CATCC--TCATTCCTAATCAAGCCATGCCATGCCAGGAGACTGGTTCCCGGTGACATCC 293
 Db 452 CGTCCATTAAAGCCCTTAAGCCCTGCTGAACACACCAACAGGGTTCCGGGTGACATCC 511
 QY 294 ATTGCTGGCAATGAGTGTGCCAGAGTTATAGTGGCAAGTTTTTCAGAA 342
 Db 512 ATTGCTGGCATAGTGTGCCAGAGTACTAGTGGCAAGTGTCTCAGAA 560

AA964962 289 bp mRNA linear EST 04-JUL-1999
 UI-R-C0-hb-c-01-0-UI.s1 UI-R-C0 Rattus norvegicus cdna clone
 UI-R-C0-hb-c-01-0-UI 3', mRNA sequence.
 AA964962
 VERSION AA964962.1 GI:4279836
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 289)
 AUTHORS Ronaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 9704477
 COMMENT On May 18, 1998 this sequence version replaced gi:3138454.
 Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 The sequence tag present in the cdna between the NotI site and the
 oligo-dT track served to identify it as a clone from the normalized
 adult 8-Day-Embryo library. cdna Library Preparation: M. Fatima
 Bonaldo, Ph.D. Clone distribution: clones will be available through
 Research Genetics This clone is also available through the
 I.M.A.G.E. Consortium at LNL (info@image.llnl.gov). IMAGE
 ID=1773166
 Seq primer: M13 Forward
 POLYA=No.


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FEATURES
  source
    Location/Qualifiers
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        /organism="Rattus norvegicus"
        /strain="Sprague-dawley"
        /db_xref="taxon:10116"
        /clone="UI-R-C0-hb-c-01-0-UI"
        /clone_lib="UI-R-C0"
        /dev_stage="adult"
        /lab_host="DH10B (Life Technologies)"
        /note="Vector: pT73D-Pac (Pharmacia) with a modified
        polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0
        library is a subtracted library derived from the UI-R-Al
        and UI-R-E1 libraries. The UI-R-Al library consisted of a
        mixture of individually tagged normalized libraries
        constructed from rat placenta, adult lung, brain, liver,
        kidney, heart, spleen, ovary, and muscle. The UI-R-E1
        library consisted of a mixture of individually tagged
        normalized libraries constructed from 8, 12 and 18-day
        embryo. The tag is a string of 3-5 nucleotides present
        between the Not I site and the oligo-dT track which
        allows identification of the library of origin of a clone
        within the mixture. The subtracted library (UI-R-C0) was
        constructed as follows: PCR amplified cDNA inserts from a
        pool of UI-R-Al and UI-R-E1 clones from which 3' ESTs had
        been derived was used as a driver in a hybridization with
        the pooled UI-R-Al and UI-R-E1 library in the form of
        single-stranded circles. The remaining single-stranded
        circles (subtracted library) was purified by
        hydroxyapatite column chromatography, converted to
        double-stranded circles and electroporated into DH10B
        bacteria (Life Technologies) to generate the UI-R-C0
        library. This procedure has been previously described
        (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
        1996)."
      70 a 56 c 67 g 96 t
      BASE COUNT
      ORIGIN
        Query Match 28.2%; Score 141.4; DB 9; Length 289;
        Best Local Similarity 78.6%; Pred. No. 1.7e-17;
        Matches 221; Conservative 0; Mismatches 51; Indels 9; Gaps 4;
      QY 152 CTGTGATTCTCATTGGGTTCACAAATTAATTCATCAAGTAATGCGCCAGCGATTAT 211
      DB 289 CTGTGATTCTCATTGGGTTCACAAATTCATCAAGTAATGCGCCAGCGATTAT 230
      QY 212 TGATCAAAATCAAAAGTAATGCATCTCTCATTCACTAAGCCATGCCATGCCAGGAGA 271
      DB 229 C-----ACGTGCGAGGCGATGATCTCCTCATCCATCAAGCCATG-CGTGACCCACAAC 177
      QY 272 CTGGTTCCCGGTGACACATCCATTGCTGGCAATGAGTGTGCGAGAGTATTAGTGCCAA 331
      DB 176 CTGGTTCCCGGTGACACATCCATTGCTGGCAATGAGTGTGCGAGATTTATTAGTGCCAA 117
      QY 332 GTTTTCACAAAGTTGAGCCACCATGGTGTGTCATGCTCATTCTTGTGAAAGCTGCCT 391
      DB 116 GTTGCTCAAAAGTCTGAAAGCACTA-AGTATGTCACAAACACTTTTGTGAAACCGCCCT 58
      QY 392 GCTCAGAGTCTATCAACATGAATATCAATGATGTCACAGAAATGG 432
      DB 57 GCTGCTGT-TGCATCATTAATAATATCAGGTGACAAACGG 18
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      BF411653/c
      LOCUS
      DEFINITION
        UI-R-BT1-Bmv-a-09-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
        UI-R-BT1-Bmv-a-09-0-UI 3', mRNA sequence.
      ACCESSION
        BF411653
      VERSION
        BF411653.1 GI:11399642
      KEYWORDS
        EST.
      SOURCE
        Norway rat.
      ORGANISM
        Rattus norvegicus
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
  1 (Bases 1 to 408)
  AUTHORS
  TITLE
  JOURNAL
  MEDLINE
  COMMENT
    Contact: Soares, MB
    Program for Rat Gene Discovery and Mapping
    University of Iowa
    451 Eckstein Medical Research Building Iowa City, IA 52242, USA
    Tel: 319 335 8250
    Fax: 319 335 9565
    Email: msoares@blue.weeg.uiowa.edu
    The sequence contained an oligo-dT track that was present in the
    oligonucleotide that was used to prime the synthesis of first
    strand cDNA and therefore this may represent a bonafide poly A
    tail. The sequence tag present in the cDNA between the NotI site
    and the oligo-dT track served to identify it as a clone from the
    normalized corpus-striatum library cDNA Library preparation: M.B.
    Soares Lab Clone distribution: clones will be available through
    Research Genetics (www.resgen.com)
    Seq primer: M13 Forward
    POLYA=Yes.
    Location/Qualifiers
      1. .408
        /organism="Rattus norvegicus"
        /strain="Sprague-Dawley"
        /db_xref="taxon:10116"
        /clone="UI-R-BT1-bmv-a-09-0-UI"
        /clone_lib="UI-R-BT1"
        /dev_stage="adult"
        /lab_host="DH10B (Life Technologies)"
        /note="Vector: pT73D-Pac (Pharmacia) with a modified
        polylinker; Site_1: Not I; Site_2: Eco RI; The library
        UI-R-BT1 is a subtracted library derived from a mixture of
        the following tissues: hippocampus, thalamus, mid-brain,
        medulla, corpus striatum, cerebral cortex and testis. For
        a detailed description of the library from which this
        clone was derived, please visit our web site at
        rated.eng.uiowa.edu. The subtraction has been previously
        described in (Bonaldo, Lennon and Soares, Genome Research
        6:791-806, 1996)
        TAG_LIB=UI-R-BT1
        TAG_TISSUE=corpus-striatum
        TAG_SEQ=CTAGG"
      BASE COUNT 120 a 82 c 83 g 123 t
      ORIGIN
        Query Match 28.0%; Score 140.2; DB 12; Length 408;
        Best Local Similarity 69.4%; Pred. No. 2.5e-17;
        Matches 284; Conservative 0; Mismatches 103; Indels 22; Gaps 6;
      QY 26 TATGCTGTATGGCTCTCAAGTGAAA--GACTTGAATTTAGTTTTTA-CCTATACCTA 82
      DB 408 TATGCTGTATGGCTCTATATGTTAAATGACITGAAAGTTAGTTCATTATCTTATGAGA 349
      QY 83 TGTCAAACTCTATTATGGAACCCCAATGGACATATGGGTTTGCACTCACACTTTTTTTTT 142
      DB 348 TGTGAAACTCTGTGTGGGACCAACAGCAGACTCTGGGTTTGA-----TTCATAC 300
      QY 143 TTTTGTTCCTGTATCTCATTTGGGTTTGCACAAATAATTCATCAAGTAATCATGGCC 202
      DB 299 TGTGTGTTCTGTGTTATCTTCACCTGGGATGGAACACAAATCGCTCAAGTACTCATGGCC 240
      QY 203 AGCATTATTGATCAAAATCAAAAGGTAATGACATCCTCATTCATCAAGCCATGCCATG 262
      DB 239 ATTGATAAT-----CAACGTCGAAGGTATCTATCATGTCATCCCACTAAGCCCATG-CTGA 187
      QY 263 CCCAGGAGACTGGTTTCCCGGTGACACATCCATTGCTGGCAATGAGTGTGCCAGAGTTAT 322
      DB 186 CCCACAACACTGGTTTCCCGGTGACACATCCCTTGTGCGCAATGAGTGTGCCAGATTCAT 127

```

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (Bases 1 to 408)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)

97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized corpus-striatum library cDNA Library preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source


```
QY 323 TAGTGCAAGTCTTTTCAGAAAGTTTGAAGCACCATGGTGTGTCATGCTCAGTCTTTGTGAA 382
|||||
Db 126 TAGTGCAAGTCTGCTCATGAAAGTCTGAAGCAGCACTAAGTATGTCACAAACACATTTTGTGRA 67
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QY 383 AGTGTCTGCTCAGAGTCTATCAACATTCGAATATCAGTGTGACAGATG 431
|||||
Db 66 AACCGGCATCCTGTTTGT-TGACATCATTAATAATCAGGTGCGATATG 19
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RESULT 12
AW915133 257 bp mRNA linear EST 25-MAY-2000
LOCUS EST346437 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
DEFINITION RGICJ89 5' end, mRNA sequence.
ACCESSION AW915133
VERSION AW915133.1 GI:8080820
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 257)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT The Institute for Genomic Research
7912, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.
FEATURES
source Location/Qualifiers
1..257
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGICJ89"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 74 a 65 c 53 g 65 t
ORIGIN
Query Match 25.7%; Score 128.6; DB 10; Length 257;
Best Local Similarity 78.1%; Pred. No. 4.9e-15;
Matches 207; Conservative 0; Mismatches 49; Indels 9; Gaps 4;

QY 161 CTCATTGGGTTGCACATAATTTCATCAAGTAATCATGCGCAGCGATTATTGATCAAAA 220
|||||
Db 2 CTCACGTGGGATTCACACAAATCCGTCAGTAGTCATGCGCAGTAGTAATC-----AA 55
|||||
QY 221 TCAAAAGGTAATGCACATCTCTATTCACTAAGCCATGCCATGCCAGGAGATGGTTTCC 280
|||||
Db 56 CGTCGAGGCATGATCATCTCATCCACTAAGCCATG-CTGACCCACAAACCTGGTTCC 114
|||||
QY 281 CGGTGACATCCATCGTGGCAATGAGTGTGCCAGATTATTAGGCCAAGTTTTCAG 340
|||||
Db 115 CGGTGACATCCATCGTGGCAATGAGTGTGCCAGATTATTAGTGCCCAAGTTGCTCAG 174
|||||
QY 341 AAGATTGAGGACCATGGTGTGTCATGCTCACTTTTGAAAGCTGCTGCTCAGAGT 400
|||||
Db 175 AAGATCTGAGGACCTA-AGTATGTCACAAACACTTTTGTGAAAACCGCCGCTGCTGCTGT 233
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QY 401 CTATCAACATTTGAATATCAGTTGAC 425
|||||
Db 234 -TGACATCATTAATAATCAGGTGAC 257
|||||
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```
RESULT 13
AA850189 246 bp mRNA linear EST 30-APR-1998
LOCUS EST192956 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
DEFINITION ROVAD66 3' end, mRNA sequence.
ACCESSION AA850189
VERSION AA850189.1 GI:2937729
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 246)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
FEATURES
source Location/Qualifiers
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/organism="Rattus sp."
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/db_xref="taxon:10118"
/clone="ROVAD66"
/clone_lib="Normalized rat ovary, Bento Soares"
/note="Organ: ovary; Vector: pT7T3pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 63 a 50 c 61 g 72 t
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Best Local Similarity 77.6%; Pred. No. 2e-13;
Matches 198; Conservative 0; Mismatches 48; Indels 9; Gaps 4;

QY 169 GGTTCGCAACAATAATTCATCAAGTAATCATGCGCAGCGATTATTGATCAAAAATCAAAAGG 228
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Db 246 GATTGCAACAACAATCCGTCAGTAGTCATGCGCAGTAGTAAT-----CAACGTCGAAG 193
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QY 229 TAATGCACATCTCATCTCACTAAGCCATGCCATGCCAGGAGACTGGTTCCCGTGACA 288
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Db 192 GCATGTACATCTCATCTCACTAAGCCATGCTGA-CCCAACACCTGGTTCCCGTGACA 134
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QY 289 CATCCATTGCTGCAATGAGTGTGCCAGATTATTAGTGCCCAAGTTTTCAGAAAGTTTG 348
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QY 349 AAGCACCATTGGTGTGTCATGCTCACTTTTGTGAAAAGCTGCTCTGCTCAGAGTCTATCAAC 408
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Db 73 AAGCACTA-AGTATGTCACAAACACTTTTGTGAAAACGCCCTGCTGTGT-TGACATC 16
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QY 409 ATTGATATCAGTTG 423
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Db 15 ATTAATATCAGGTG 1
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RESULT 14
AZ310595 483 bp DNA linear GSS 29-SEP-2000
LOCUS IM0025E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0025E11 R, DNA sequence.
ACCESSION AZ310595
VERSION AZ310595.1 GI:10352738
KEYWORDS GSS.
SOURCE house mouse.
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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1 (bases 1 to 483)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0025 row: E column: 11
Seq primer: CACACAGGAAACAGCTATCACC
Class: plasmid ends
High quality sequence scop: 483.
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            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[g14732114]a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      138 a 110 c 96 g 139 t
ORIGIN
Query Match      21.8%; Score 109; DB 17; Length 483;
Best Local Similarity 77.6%; Pred. No. 2.2e-11;
Matches 201; Conservative 0; Mismatches 40; Indels 18; Gaps 5;
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QY 59 AATTAGTTTTTACC-TATACCTATGTGAACACTTATTATGGAAACCAATGACATATG 117
Db 184 AAGTAGTTCATTACCTTATACAGATGTGAACACTCTGGTGGTGAACCAAGCAGAC-TCGTG 126
QY 118 GGTTCGAACACACTTTTTTTTTTTTGTCTGTGTATTCATCTGGGTGCAAC 177
Db 125 GGTTCGAACACACT-----TTTTTTGTCTGTGTATTCATCTAGATGTCAC 74
QY 178 AATAATTCATCAAGTAATCATGCCAGGATTTATGATCAAAATCAAAAGTAAATGCACA 237

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Db 73 AACAGTCTATCAATAGTATGCGCCAGTGATAAT-----CAAAGTCAAAGGCACACACA 20
QY 238 TCCCTCATTCACATAGCCAT 256
Db 19 TCCCTCGTCCCATTAAGCCAT 1
RESULT 15
BH290554      634 bp DNA linear GSS 30-NOV-2001
LOCUS      CH230-78A16.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
DEFINITION      CH230-78A16, DNA sequence.
ACCESSION      BH290554
VERSION      BH290554.1 GI:17202962
KEYWORDS      GSS.
SOURCE      Norway rat.
ORGANISM      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 634)
AUTHORS      Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn
,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de
Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-78A16.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 78 row: A column: 16
Seq primer: SP6
Class: BAC ends.
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            /db_xref="taxon:10116"
            /clone="CH230-78A16"
            /clone_lib="CHORI-230 Segment 1"
            /sex="Female"
            /cell_type="Brain"
            /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT      175 a 138 c 146 g 175 t
ORIGIN
Query Match      19.0%; Score 95.2; DB 17; Length 634;
Best Local Similarity 75.7%; Pred. No. 8.4e-09;
Matches 162; Conservative 0; Mismatches 38; Indels 14; Gaps 3;
QY 1 TTACAGGGCAGTGGCTTTGTAGCTATGCTGTGTATGGCTCTCAAGTGAAA--GACTTG 58
Db 386 TTACAGGGCAGTGGCTTTGTAGCTATGCTGTGTATGGCTCTCAAGTGAAAATGACTTG 445
QY 59 AATTAGTTTTTAA-CCATACCTATGTAACACTTATTATGGAAACCAATGACATATG 117
Db 446 AAGTAGTTCATTATCTATGATGCATGTGAACACTCTGGTGGTGAACCAAGCAGACTCTGG 505
QY 118 GGTTCGAACACACTTTTTTTTTTTTGTCTGTGTATTCATCTGGGTGCAAC 177
Db 506 GTTTTGA-----TTCACTACTGTTTGTCTGTATTCCTCACTGGATGCAC 554

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QY 178 AATAATTCATCAAGTAATCATGGCCACCGATTAT 211
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Db 555 AACAAATCCGTCAAGTAGTAGTAATGGCCAATGATAAT 588

Search completed: April 3, 2003, 16:37:00
Job time : 572.323 secs

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 1539.86 Seconds
(without alignments)
14684.987 Million cell updates/sec

Title: US-09-595-526c-1_COPY_9500_10276

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
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- 8: gb_pl.*
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- 14: gb_vt.*
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- 38: em_sy.*
- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	773	99.5	3366	6	AX060718	Sequence
2	773	99.5	3366	6	AX060897	Sequence
3	773	99.5	10442	6	AX060713	Sequence
4	773	99.5	10442	6	AX060892	Sequence
5	773	99.5	10442	9	AF285167	Sequence
6	773	99.5	10474	6	AX060719	Sequence
7	773	99.5	10474	6	AX060721	Sequence
8	773	99.5	10474	6	AX060898	Sequence
9	773	99.5	10474	6	AX060900	Sequence
10	688	88.5	149034	9	AF275948	Sequence
11	688	88.5	182012	9	AF275948	Sequence
12	688	88.5	201144	9	AF287262	Sequence
13	673	86.6	183999	9	AX092589	Sequence
14	666	85.7	3501	6	AX059896	Sequence
15	666	85.7	5352	6	AX127778	Sequence
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18	664.2	85.5	5097	9	AK027864	Homo sapi
19	664.2	85.5	5097	23	BD005026	Genes rel
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21	335	43.1	2264	6	AX059972	Sequence
22	331	42.6	1237	6	AX059929	Sequence
23	331	42.6	2617	6	AX059974	Sequence
24	331	42.6	2894	6	AX127797	Sequence
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26	331	42.6	9495	6	AX059978	Sequence
27	331	42.6	9497	6	AX059973	Sequence
28	331	42.6	9497	9	AF165281	Homo sapi
29	331	42.6	9593	6	AX059976	Sequence
30	331	42.6	9741	6	AX127830	Sequence
31	331	42.6	9741	6	AX139817	Sequence
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37	280.4	36.1	186889	2	AL807243	Mus muscu
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43	50.4	6.5	85779	8	SCE011856	Saccharom
44	50.2	6.5	1141	6	AX083744	Sequence
45	49.2	6.3	82469	2	AC116330	Diclyoste

ALIGNMENTS

RESULT 1	AX060718	Sequence	3366 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060718	Sequence	6 from Patent WO0078972.			
DEFINITION	AX060718					
ACCESSION	AX060718					
VERSION	AX060718.1	GI:12406107				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 3366)					
AUTHORS	Lawn,R.M., Wade,D. and Garvin,M.					
TITLE	Regulation with binding cassette transporter protein abcl					
JOURNAL	Patent: WO 0078972-A 6 28-DEC-2000;					

Pred. No. is the number of results predicted by chance to have a

FEATURES	CV THERAPEUTICS, INC. (US)
source	Location/Qualifiers 1..3366 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	1119 a 564 c 559 g 1120 t 4 others
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Best Local Similarity	100.0%; Pred. No. 6.9e-142;
Matches 777; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy 1	GTAACCTAATTCGCTAGAAATTTTACCACACTCTATCTCAATCAAGCAAATTTCTGTG 60
Db 2424	GTAACCTAATTCGGTAGAAATTTTACCACACTCTATCTCAATCAAGCAAATTTCTGTG 2483
Qy 61	TATATCCCTCGGAATGTACTATGTGAGTTTTCAGAAAATTCATAAATACGTTGTCAAA 120
Db 2484	TATATCCCTCGGAATGTACCTATGTGAGTTTTCAGAAAATTCATAAATACGTTGTCAAA 2543
Qy 121	AATTTCGTCTTTGCATCTCTTTGGACACCTCAGAAAACTTATTAAACAACGTGGAATATGA 180
Db 2544	AATTTCGTCTTTGCATCTCTTTGGACACCTCAGAAAACTTATTAAACAACGTGGAATATGA 2603
Qy 181	GAATACAGAAGAAATAATAAGGCCCTCTAFACATAAATGCCAGCACAAATTCATTGTGTA 240
Db 2604	GAATACAGAAGAAATAATAAGGCCCTCTATACATAAATGCCAGCACAAATTCATTGTGTA 2663
Qy 241	AAAAACAACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGTAAAGCAAAATGCTTTG 300
Db 2664	AAAAACAACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGTAAAGCAAAATGCTTTG 2723
Qy 301	TGACTATTAATGTGCACATCATCTACTGTATAGTAATCAATTCACACTAAAGGCCAATT 360
Db 2724	TGACTATTAATGTGCACATCATCTACTGTATAGTAATCAATTCACACTAAAGGCCAATT 2783
Qy 361	TGCTGTGTTTTCTCTTTTGSGNTGNATATATCAGSTAAAATATTTTCCAAGAGCCCAATGT 420
Db 2784	TGCTGTGTTTTCTCTTTTGSGNTGNATATATCAGSTAAAATATTTTCCAAGAGCCCAATGT 2843
Qy 421	GTCAATTAATCTGAACCCCTTGATATTGACATTAATTGGACCCCTTGGTATATCTA 480
Db 2844	GTCAATTAATCTGAACCCCTTGATATTGACATTAATTGGACCCCTTGGTATATCTA 2903
Qy 481	CTAGAATAATGTAACTACTGNAGAAATATTCGTCTAAATCTTTTCAAAATGGTGCATCCCC 540
Db 2904	CTAGAATAATGTAACTACTGNAGAAATATTCGTCTAAATCTTTTCAAAATGGTGCATCCCC 2963
Qy 541	TTAAANGTTCTATTTCCTAAGGATTTAGTTGCTTATCCCTTCTTATACCCCTAAGATG 600
Db 2964	TTAAANGTTCTATTTCCTAAGGATTTAGTTGCTTATCCCTTCTTATACCCCTAAGATG 3023
Qy 601	AAGCTGTTTTTGCTCTTTGTTTCATCATTTGGCCCTCATTCCTCAAGACACTTTACGCTGTCT 660
Db 3024	AAGCTGTTTTTGCTCTTTGTTTCATCATTTGGCCCTCATTCCTCAAGACACTTTACGCTGTCT 3083
Qy 661	GTAATGGGATCTATTTTTCGACTGGAAATATCTGAGAATTCGAAAACCTAGACAAAGTTTC 720
Db 3084	GTAATGGGATCTATTTTTCGACTGGAAATATCTGAGAATTCGAAAACCTAGACAAAGTTTC 3143
Qy 721	ACACAGATTTCTAAGTTAATCATTTTCAATTAAGGAAAAAGAAAAATTTT 777
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RESULT 2	
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LOCUS	AX060897 3366 bp DNA linear PAT 22-JAN-2001
DEFINITION	Sequence 6 from Patent WO0078971.
ACCESSION	AX060897
VERSION	AX060897.1 GI:12406274
KEYWORDS	human;
SOURCE	

AX060713	AX060713	10442 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	Sequence 1 from Patent WO0078972.				
DEFINITION	Sequence 1 from Patent WO0078972.				
ACCESSION	AX060713				
VERSION	AX060713.1	GI:12406103			
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Lawn, R.M., Wade, D. and Garvin, M.				
TITLE	Regulation with binding cassette transporter protein abcl				
JOURNAL	Patent: WO 0078972-A 1 28-DEC-2000;				
	CV THERAPEUTICS, INC. (US)				
FEATURES	Location/Qualifiers				
source	1..10442				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
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ORIGIN	4 others				
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Best Local Similarity	100.0%; Pred. No. 5.5e-142;				
Matches	777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 GTAAACCTAAATGCGTAGAATAATTTTACCAACTCTATACCTCAATCAAGCAAAATTTCTG 60				
Db	9500 GTAAACCTAAATGCGTAGAATAATTTTACCAACTCTATACCTCAATCAAGCAAAATTTCTG 9559				
QY	61 TATATTCCTCTGGAAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTTGTCAAA 120				
Db	9560 TATATTCCTCTGGAAATGTACCTATGTGAGTTTCAGAAATTTCTCAAAATACGTTGTCAAA 9619				
QY	121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTTATTAACTACTGTGAATATGA 180				
Db	9620 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTTATTAACTACTGTGAATATGA 9679				
QY	181 GAAATACAGAAGAAAATAAATAGGCCCTCTATACATATAATGCCAGCAAAATTCATTGTGA 240				
Db	9680 GAAATACAGAAGAAAATAAATAGGCCCTCTATACATATAATGCCAGCAAAATTCATTGTGA 9739				
QY	241 AAAAACACCAAACTCACACTACTGTATTTCATTTATCTGACTGAAAGCAAAATGCTTTG 300				
Db	9740 AAAAACACCAAACTCACACTACTGTATTTCATTTATCTGACTGAAAGCAAAATGCTTTG 9799				
QY	301 TGACTATTAAATGTTGGACATCAATTCACCTGTATAGTAATCATTCACCTAAAGCCCAAT 360				
Db	9800 TGACTATTAAATGTTGGACATCAATTCACCTGTATAGTAATCATTCACCTAAAGCCCAAT 9859				
QY	361 TGCTGTGTTTCTCTTCTGTGNTGNATATATCAGGTAAAAATATTTCCAAAGAGCCATGT 420				
Db	9860 TGCTGTGTTTCTCTTCTGTGNTGNATATATCAGGTAAAAATATTTCCAAAGAGAGCCATGT 9919				
QY	421 GTCATGTAATACCTGAACCCCTTGATTTGACACATTAATTTGGACCCCTTGTTATTATCTA 480				
Db	9920 GTCATGTAATACCTGAACCCCTTGATTTGACACATTAATTTGGACCCCTTGTTATTATCTA 9979				
QY	481 CTAGAATAATGTAATACCTGNAGAAATATTTGCTTAATTTCTTCAAAATGGTGCAATCCCCC 540				
Db	9980 CTAGAATAATGTAATACCTGNAGAAATATTTGCTTAATTTCTTCAAAATGGTGCAATCCCCC 10039				
QY	541 TTAAAGNTTCTATTTCCATAGGAATTTAGCTTGCTTATCCCTTCTTATACCTCAAGATG 600				
Db	10040 TTAAAGNTTCTATTTCCATAGGAATTTAGCTTGCTTATCCCTTCTTATACCTCAAGATG 10099				
QY	601 AAGCTGTTTTTGTGCTCTTTGTTTCATCATTTGGCCCTCATTTCCAAGCACTTTACGGTGTCT 660				
Db	10100 AAGCTGTTTTTGTGCTCTTTGTTTCATCATTTGGCCCTCATTTCCAAGCACTTTACGGTGTCT 10159				
QY	661 GTAATGGGATCTATTTTTCGACTGGAAATATCTGAGAAATGCAAACTAGACAAAGATTTC 720				
Db	10160 GTAATGGGATCTATTTTTCGACTGGAAATATCTGAGAAATGCAAACTAGACAAAGATTTC 10219				

Qy	721	ACAACAGATTCTTAAGTTTAAATCAATTTTCATTAAGAGGAAAGAAAAATTTT	777
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RESULT 4			
AX060892			
LOCUS	AX060892	10442 bp	linear
DEFINITION	Sequence 1 from Patent WO0078971.		PAT 22-JAN-2001
ACCESSION	AX060892		
VERSION	AX060892.1	GI:12406270	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 10442)		
JOURNAL	Law, R.M., Wade, D., Oram, J.F. and Garvin, M.		
FEATURES	Atp binding cassette transporter protein abcl polypeptides		
Source	Patent: WO 0078971-A 1 28-DEC-2000;		
	CV THERAPEUTICS, INC. (US)		
	Location/Qualifiers		
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	/db_xref="taxon:9606"		
BASE COUNT	2898 a 2297 c 2408 g 2835 t		
ORIGIN			
	Query Match 99.5%; Score 773; DB 6; Length 10442;		
	Best Local Similarity 100.0%; Pred. No. 5.5e-142;		
	Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	GTAACCTAATTCGGTGAAGAAATTTTACCACCTCTATACCTCAATCAAGCAAAATTTCTG	60
Db	9500	GTAACCTAATTCGGTGAAGAAATTTTACCACCTCTATACCTCAATCAAGCAAAATTTCTG	9559
Qy	61	TATATTCCTCGTGGAAATGACCTATGTGAGTTTCAGAAATTCCTCAAAATACGCTGTCAAA	120
Db	9560	TATATTCCTCGTGGAAATGACCTATGTGAGTTTCAGAAATTCCTCAAAATACGCTGTCAAA	9619
Qy	121	AAATTCTCGTTTGGCATCTTTGGGACACCTCAGAAACCTTATTACAACTGTGTAATGA	180
Db	9620	AAATTCTCGTTTGGCATCTTTGGGACACCTCAGAAACCTTATTACAACTGTGTAATGA	9679
Qy	181	GAATACAGAGAAAAATTAATAGCCCTCTATACATAAAATGCCAGCACAAATTCATTGTA	240
Db	9680	GAATACAGAGAAAAATTAATAGCCCTCTATACATAAAATGCCAGCACAAATTCATTGTA	9739
Qy	241	AAACACACCAACCTCCACCTACCTGTAATTCATTATCTGTACTGAAGCAAAATGCTTTG	300
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Qy	481	CTAGATATATGTAATACCTGNAGAAATATGGCTCAATTTCTTCAAAATGGTGCATCCCC	540
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RESULT 6
AX060719 AX060719 10474 bp DNA linear PAT 22-JAN-2001
LOCUS Sequence 7 from Patent WO0078972.
DEFINITION AX060719
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source Location/Qualifiers
1..10474
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/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN
Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Sequence 9 from Patent WO0078972.
DEFINITION AX060721
ACCESSION AX060721
VERSION AX060721.1 GI:12406109
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D. and Garvin,M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
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/db_xref="taxon:9606"
BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
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Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 9652 AATTTCGCTTTTGCATCTTTGGACACCTCAGAAAATTTTAAACAACTGTGAATATGA 9711
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RESULT 8
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LOCUS AX060898 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 7 from Patent WO0078971.
ACCESSION AX060898
VERSION AX060898.1 GI:12406275
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 7 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 2906 a 2305 c 2416 g 2843 t 4 others
ORIGIN
Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTGTAGAAATTTTACCACCTCTATCTCAATCAATCAAGCAAAATTTCTG 60
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Db 9592 TATATCCCTGTGGATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGTTTCAA 9651
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAACTGTGAATATGA 180
Db 9652 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAACTGTGAATATGA 9711
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RESULT 9
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LOCUS AX060900 10474 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 9 from Patent WO0078971.
ACCESSION AX060900
VERSION AX060900.1 GI:12406276
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10474)
AUTHORS Lawn,R.M., Wade,D., Oram,J.F. and Garvin,M.
TITLE Atp binding cassette transporter protein abcl polypeptides
JOURNAL Patent: WO 0078971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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BASE COUNT 2907 a 2304 c 2415 g 2844 t 4 others
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Query Match 99.5%; Score 773; DB 6; Length 10474;
Best Local Similarity 100.0%; Pred. No. 5.5e-142;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTGTAGAAATTTTACCACCTCTATCTCAATCAATCAAGCAAAATTTCTG 60
Db 9532 GTAAACCTAATTTGGTGTAGAAATTTTACCACCTCTATCTCAATCAATCAAGCAAAATTTCTG 9591
QY 61 TATATCCCTGTGGATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGTTTCAA 120
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QY	301	TCACATTAATAATGTTGCACATCATTCATCTACTGTATAGTAATCATTTGACTAAGCCATT	360
DB	9832	TCACATTAATAATGTTGCACATCATTCATCTACTGTATAGTAATCATTTGACTAAGCCATT	9891
QY	361	TCCTGTGTTTTCTCTCTGTTGTTGNATATATACAGTAAATATATTTCCAAAGAGCCATGT	420
DB	9892	TCCTGTGTTTTCTCTCTGTTGTTGNATATATACAGTAAATATATTTCCAAAGAGCCATGT	9951
QY	421	GTCATGTAATACAGCCCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTA	480
DB	9952	GTCATGTAATACAGCCCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTA	10011
QY	481	CTAGTAATATGTAATACAGTAAATATATGCTCTAAATCTTTCAAAATGTCATCCCCC	540
DB	10012	CTAGTAATATGTAATACAGTAAATATATGCTCTAAATCTTTCAAAATGTCATCCCCC	10071
QY	541	TTAAANAGTTCTATTTCCATTAAGGATTTAGTCTTATCCCTTCTTATACCCCTAAGATG	600
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DB	10132	AGCTGTTTTGTCCTCTTTGTCATCATGTCCTCATCCCAAGCACTTTAGCTGTCT	10191
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DB	10192	GTAATGGGATCTATTTTGCATCGAATATCTGAGAATTCGAAATAGACAAAAGTTTC	10251
QY	721	ACAACAGATTTCTAGTTAAATCATTTTCATTAAGGAAAGAAAGAAAATTTT	777
DB	10252	ACAACAGATTTCTAGTTAAATCATTTTCATTAAGGAAAGAAAGAAAATTTT	10308
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LOCUS	AF275948	149034 bp DNA linear PRI 17-JUL-2000	
DEFINITION	Homo sapiens ABCA1 (ABCA1) gene, complete cds.		
ACCESSION	AF275948		
VERSION	AF275948.1	GI:9247085	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 149034) Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Cheng,J.F., Osorio,J., Renaley,A., Yang,X.P., Haudenschild,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Deneffe,P., Fredrickson,D.S. and Brewer,H.B. Jr.		
TITLE	Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)		
MEDLINE	20345099		
PUBMED	10894428		
REFERENCE	2 (bases 1 to 149034) Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A., Renaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E., Francois,T.L. and Brewer,H.B. Jr.		

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and SNAP protein genes, complete cds.
ACCESSION AF287262
VERSION AF287262.1 GI:13876612
KEYWORDS SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201144)
AUTHORS Qiu,X., Cavellier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F.
TITLE Human and mouse ABCA1 comparative sequencing and transgenesis
studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
JOURNAL MEDLINE 21251004
PUBMED 11352567
REFERENCE 2 (bases 1 to 201144)
AUTHORS Qiu,X., Cavellier,L., Chiu,S., Rubin,E. and Cheng,J.F.
TITLE Direct Submission

FEATURES

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Location/Qualifiers

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LOCUS
DEFINITION Sequence 14 from Patent WO0078970.
ACCESSION AX059896
VERSION AX059896.1 GI:12405554
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Assmann,G., Rust,S., Funke,H.
and Brewer,H.B.
TITLE Nucleic and proteinic acids corresponding to human gene abcl
JOURNAL Patent: WO 0078970-A 14 28-DEC-2000;
Aventis Pharma S.A. (FR)
FEATURES
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BASE COUNT 1139 a 595 c 598 g 1169 t
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Best Local Similarity 96.8%; Pred. No. 6.2e-121;
Matches 763; Conservative 0; Mismatches 14; Indels 11; Gaps 8;
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LOCUS
DEFINITION Sequence 17 from Patent WO0130848.
ACCESSION AX127778
VERSION AX127778.1 GI:14134425
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE
AUTHORS Denefle,P., Rosier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
TITLE Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
JOURNAL Patent: WO 0130848-A 17 03-MAY-2001;
Aventis Pharma S.A. (FR)
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BASE COUNT 1575 a 928 c 976 g 1772 t
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Query Match      85.7%; Score 666; DB 6; Length 5352;
Best Local Similarity 96.8%; Pred. No. 5.7e-121;
Matches 763; Conservative 0; Mismatches 14; Indels 11; Gaps 8;

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Db 3118 TGCTGTGTTTTCTTCTGTGGTGNATATATCAGGTAAATAATTTTCCAAAGACCATG 3177

QY 420 TGTCATGTAATCTGAACC-CTTTGATATGAGACATTAATTTGGACCT-TGCTATTAT 477
Db 3178 TGTCATGTAATCTGAACCCTTTGATATGAGACATTAATTTGGACCTGCTATTAT 3237

QY 478 CTACTAG-AAATATGTAATCTGNAGAAATATGCTCTAATCTTTT--CAAAATGGTGCA 534
Db 3238 CTACTAGTAATAATGTAATCTAGAAATATGCTCTAATCTTTTCAAAATTTGTTGCA 3297

QY 535 TCCCCCTTAAANG-TTCTATTCCATAGGATTAGCT---TGCTTATCCCTTCTTATA 590
Db 3298 TCCCCCTTAGAATGTTCTATTTCATAGGATTTAGGTATGCTATTATCCCTTCTTATA 3357

QY 591 CCCTAAGATGAAGCTGTTTTTGTGCTCTTTGTTTCATCATGCGCCCTCATTCGAAGCACTT 650
Db 3358 CCCTAAGATGAAGCTGTTTTTGTGCTCTTTGTTTCATCATGCGCCCTCATTCGAAGCACTT 3417

QY 651 TAGCGTCTGTGAATGGGATCTATTTTGCACCTGGAATATCTCAGAAATTCGAAACTAGA 710
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QY 711 CAAAAGTTTCACACAGA-TTCTAAGTTAAATCAATTTTCAATTAAGGAAAAAGAAAA 769
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Run on: April 3, 2003, 09:40:44 ; Search time 130.719 Seconds
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	773	99.5	3366	22 AAF24684	Nucleotide sequenc
2	773	99.5	3366	22 AAF24706	Nucleotide sequenc
3	773	99.5	10442	22 AAF24680	Nucleotide sequenc
4	773	99.5	10442	22 AAF24702	Nucleotide sequenc
5	773	99.5	10474	22 AAF24685	Nucleotide sequenc
6	773	99.5	10474	22 AAF24686	Nucleotide sequenc
7	773	99.5	10474	22 AAF24707	Nucleotide sequenc
8	773	99.5	10474	22 AAF24708	Nucleotide sequenc
9	673	86.6	183999	22 AAF92831	Human ABC1 genomic

10 666 85.7 5352 22 AAS04049 Human ABC1 gene, p
11 664.2 85.5 5097 22 AA193913 Human stomach canc
12 664.2 85.5 5097 22 AAH18233 Human cDNA sequenc
13 494.4 63.6 601 24 ABN94924 Gene #1422 used to
14 427.2 55.0 554 22 AAH13302 Human cDNA clone (

C 15 331 42.6 9741 22 AAS06120 Human ABC1 DNA seq
16 331 42.6 9741 22 AAS37273 Human ABC1 full-le
17 331 42.6 9854 22 AAS06121 Human ABC1 DNA seq
18 327 42.1 451 24 ABL63621 Breast cancer rela
19 327 42.1 451 24 ABL64032 Breast cancer rela
20 152 19.6 329 24 ABN94208 Gene #706 used to
21 110 14.2 210 16 AAT22245 Human gene signatu
22 47.2 6.1 7500 24 ABL33114 Human immune syste
23 46.6 6.0 7195 22 AAS43324 Chemically pretrea
24 46.2 5.9 5523 24 ABL32165 Human immune syste
25 46.2 5.9 5457 24 ABL33131 Human immune syste
26 45.6 5.9 5986 24 AAS61432 Human gene regulat
27 45.6 5.9 5986 24 ABK31498 Signal transductio
28 45.2 5.8 700 22 AAH93026 Human inflammatory
29 45.2 5.7 16170 24 ABL33269 Human immune syste
30 44.6 5.7 11209 24 ABN80137 Human chemically m
31 44.2 5.7 19087 24 ABL32793 Human immune syste
32 44.2 5.7 6169 22 AAS46369 Tumour suppressor
33 44 5.7 6169 24 ABN80096 Human chemically m
34 43.8 5.6 9652 24 ABL32909 Human immune syste
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41 43.2 5.6 83391 24 ABQ67094 Human angiogenesis
42 43.2 5.6 103929 21 AAF22287 BAC containing rep
43 43.2 5.5 154902 24 ABQ88198 Human osteoblast d
44 42.6 5.5 168575 22 AAH21613 Human hypocrerin r

ALIGNMENTS

RESULT 1
AAF24684

ID AAF24684 standard; DNA; 3366 BP.

XX AAF24684;

XX AAF24684;

DT 20-APR-2001 (first entry)

XX Nucleotide sequence of the 3' flanking region of the human ABC1 gene.

DE Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

XX KW chromosome 9q22-q31; heart disease; hypercholesterolemia;

XX KW atherosclerosis; cholesterol transport; ss.

OS Homo sapiens.

XX WO200078972-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US16765.

XX 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

PR 19-NOV-1999; 99US-0166573.

XX (CVTH-) CV THERAPEUTICS INC.

XX Lawn RM, Wade D, Garvin M;

XX WPI; 2001-137812/14.

XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
PS Disclosure; Page 146-148; 215pp; English.
XX
CC The present sequence represents the 3' flanking region of the human
CC adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1
CC resides in cell membranes and utilizes ATP hydrolysis to transport a wide
CC variety of substrates across the plasma membrane. ABC1 is a pivotal
CC protein in the apolipoprotein-mediated mobilisation of intracellular
CC cholesterol stores. ABC1 is defective in Tangier disease, a genetic
CC disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
CC gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins
CC are useful for developing pharmaceutical agents for the treatment of
CC heart disease and other disorders associated with hypercholesterolemia
CC and atherosclerosis. The genes are useful for developing screening assays
CC to screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
SQ Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

Query Match 99.5%; Score 773; DB 22; Length 3366;
Best Local Similarity 100.0%; Pred. No. 8.3e-165;
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2424 GTAACCTAATTCGTGAGAAATTTTACCACTCTATCTCAATCAACGAAATTTCTG 2483

QY 61 TATATCCCTGCGAATGATACCTATGAGTTTCAGAAATTTTCAAAATACGTTTCAA 120
DB 2484 TATATCCCTGCGAATGATACCTATGAGTTTCAGAAATTTTCAAAATACGTTTCAA 2543

QY 121 AATTCGTGCTTTTGCATCTTTGGGACACTCAGAAACATTTATCAACATGCAATAGA 180
DB 2544 AATTCGTGCTTTTGCATCTTTGGGACACTCAGAAACATTTATCAACATGCAATAGA 2603

QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGA 240
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QY 241 AAAACAACCAACCTCACACTACTGTTATTCATATCTGCTACTGAAACCAATGCTTG 300
DB 2664 AAAACAACCAACCTCACACTACTGTTATTCATATCTGCTACTGAAACCAATGCTTG 2723

QY 301 TGACTATTAAATGTTGCATCATTCATTCACCTGTATAGTATATCATTCAGTAAAGCCATT 360
DB 2724 TGACTATTAAATGTTGCATCATTCATTCACCTGTATAGTATATCATTCAGTAAAGCCATT 2783

QY 361 TGTGCTTTTCTTCTGTTGGTGNATATATACAGGTAATAATTTTCCAAAGAGCATGT 420
DB 2784 TGTGCTTTTCTTCTGTTGGTGNATATATACAGGTAATAATTTTCCAAAGAGCATGT 2843

QY 421 GTCATGTAATACCTGAACCTTTGATATTCAGACATTAATTTGGACCTTGGTATTATCTA 480
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QY 481 CTAGAATAATGTAATACCTGNAGAAATATTGCTCTAATTTCTTCAAAGGTCATCCCCC 540
DB 2904 CTAGAATAATGTAATACCTGNAGAAATATTGCTCTAATTTCTTCAAAGGTCATCCCCC 2963

QY 541 TTAAGAAGTCTATTTCCTAAGCAATTAAGCTTGTGCTTATCCCTCTTATACCTTAAGTG 600
DB 2964 TTAAGAAGTCTATTTCCTAAGCAATTAAGCTTGTGCTTATCCCTCTTATACCTTAAGTG 3023

QY 601 AAGCTGTTTTGTGCTTTTGTGTCATTCATTCGCTCATTCAGCAACATTTACGCTGCT 660
DB 3024 AAGCTGTTTTGTGCTTTTGTGTCATTCATTCGCTCATTCAGCAACATTTACGCTGCT 3083

QY 661 GTAATGGGATCTATTTTCCACTGGAATATCTGAGAATTCGAAACTAGACAAAAGTTTC 720
DB 3084 GTAATGGGATCTATTTTCCACTGGAATATCTGAGAATTCGAAACTAGACAAAAGTTTC 3143

QY 721 ACAACAGATTTCTTAAGTTAAATCATTTTCATTAAGGAGAAAGAAAAAATTTT 777
DB 3144 ACAACAGATTTCTTAAGTTAAATCATTTTCATTAAGGAGAAAGAAAAAATTTT 3200

RESULT 2

AAF24706
ID AAF24706 standard; DNA; 3366 BP.

AC AAF24706;

DT 20-APR-2001 (first entry)

XX Nucleotide sequence of the 3' flanking region of the human ABC1 gene.
DE Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX

OS Homo sapiens.

PN WO200078971-A2.

PD 28-DEC-2000.

PF 16-JUN-2000; 2000WO-US16591.

PR 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

PR 19-NOV-1999; 99US-0166573.

XX (CVTH-) CV THERAPEUTICS INC.

PA (UNIW) UNIV WASHINGTON.

PI Lawn RM, Wade D, Oram JF, Garvin M;

XX WPI; 2001-137811/14.
XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
PT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX

PS Disclosure; Page 142-144; 211pp; English.

XX The present sequence represents the 3' flanking region of the human
XX adenosine triphosphate (ATP) binding cassette protein (ABC) 1 gene. ABC1
XX resides in cell membranes and utilizes ATP hydrolysis to transport a wide
XX variety of substrates across the plasma membrane. ABC1 is a pivotal
XX protein in the apolipoprotein-mediated mobilisation of intracellular
XX cholesterol stores. ABC1 is defective in Tangier disease, a genetic
XX disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1
XX gene is localised to chromosome 9q22-9q31. The ABC1 genes and proteins
XX are useful for developing pharmaceutical agents for the treatment of
XX heart disease and other disorders associated with hypercholesterolemia
XX and atherosclerosis. The genes are useful for developing screening assays
XX to screen for compounds that regulate the expression of genes associated
XX with cholesterol transport. The genes and proteins are also useful for
XX are also useful as diagnostic indicators of cardiovascular disease and
XX other disorders associated with hypercholesterolemia.

SQ Sequence 3366 BP; 1119 A; 564 C; 559 G; 1120 T; 4 other;

Query Match 99.5%; Score 773; DB 22; Length 3366;

Best Local Similarity 100.0%; Pred. No. 8.3e-165;

Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTAAACCTAATGTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
Df 2424 GTAACCTAATGTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2483
QY 61 TATATTCCTGTGGAATGACCTATGAGTTTCAGAAATTTCTCAAAATACGTGTTCAAA 120
Df 2484 TATATTCCTGTGGAATGACCTATGAGTTTCAGAAATTTCTCAAAATACGTGTTCAAA 2543
QY 121 AATTCCTGTTTGGCACTTTGGGACACCTCAGAAACTTATTAACAACCTGTGAATATGA 180
Df 2544 AATTCCTGTTTGGCACTTTGGGACACCTCAGAAACTTATTAACAACCTGTGAATATGA 2603
QY 181 GAATACAGAGAAATTAATAAGCCCTCTATACATAATGCCAGACACATTCATTGTTA 240
Df 2604 GAATACAGAGAAATTAATAAGCCCTCTATACATAATGCCAGACACATTCATTGTTA 2663
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Df 2664 AAAACACCAACCTCACACTACTGCTATTCATTATCTGCTAGTGAAGCAAAATGCTTTC 2723
QY 301 TGACTATTAATGTGCACATCAATTCATTCACCTGATAGTAATCATGTAGTAAGCCATT 360
Df 2724 TGACTATTAATGTGCACATCAATTCATTCACCTGATAGTAATCATGTAGTAAGCCATT 2783
QY 361 TGCTGTGTTTCTCTTGTGNTGNATATATCAGTAAATATTTTCCAAAGAGCCATGT 420
Df 2784 TGCTGTGTTTCTCTTGTGNTGNATATATCAGTAAATATTTTCCAAAGAGCCATGT 2843
QY 421 GTCATGTAATACGACCCCTTGATATGAGACATTAATTTGGACCCCTGGTATTAATCTA 480
Df 2844 GTCATGTAATACGACCCCTTGATATGAGACATTAATTTGGACCCCTGGTATTAATCTA 2903
QY 481 CTAGAAATATGTAATCTAGTGNAGAAATATGCTCTAATTTCTTCAAAATGTCATCCCCC 540
Df 2904 CTAGAAATATGTAATCTAGTGNAGAAATATGCTCTAATTTCTTCAAAATGTCATCCCCC 2963
QY 541 TTAAGGTTCTAATTTCCATGAAGATTTAGCTGCTTATCCCTTCTTATACCCCTAGATG 600
Df 2964 TTAAGGTTCTAATTTCCATGAAGATTTAGCTGCTTATCCCTTCTTATACCCCTAGATG 3023
QY 601 AAGCTGTTTGTGCTCTTTGTCATCATTTGGCCCTCATTCAGACACTTTACGCTGTCT 660
Df 3024 AAGCTGTTTGTGCTCTTTGTCATCATTTGGCCCTCATTCAGACACTTTACGCTGTCT 3083
QY 661 GTAATGGATCTAATTTTGGACGGAATATCTGAGAAATGCAAACTAGACAAAGTTTC 720
Df 3084 GTAATGGATCTAATTTTGGACGGAATATCTGAGAAATGCAAACTAGACAAAGTTTC 3143
QY 721 ACAACAGATTTCTAAGTTAAATCATTTTCAATTAAGGAAAGAAAGAAATTTT 777
Df 3144 ACAACAGATTTCTAAGTTAAATCATTTTCAATTAAGGAAAGAAAGAAATTTT 3200

RESULT 3
AAF24680
ID AAF24680 standard; DNA; 10442 BP.
XX AC AAF24680;
XX 20-APR-2001 (first entry)
XX Nucleotide sequence of a human ABC1 polypeptide.
XX Human: adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX OS Homo sapiens.
XX PH Key
XX CDS 291..7076
XX FT /*tag= a
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FT /product= "ABC1 polypeptide"
PN WO200078972-A2.
XX 28-DEC-2000.
XX 16-JUN-2000; 2000WO-US16765.
XX 18-JUN-1999; 99US-0140264.
PR 14-SEP-1999; 99US-0153872.
PR 19-NOV-1999; 99US-0166573.
XX (CVTH-) CV THERAPEUTICS INC.
XX Lawn RM, Wade D, Garvin M;
XX WPI; 2001-137812/14.
XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
PT useful for the development of agents for the treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX Disclosure; Page 122-128; 215pp; English.
XX The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC are also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
XX Query Match 99.5%; Score 773; DB 22; Length 10442;
XX Best Local Similarity 100.0%; Pred. No. 1e-164;
XX Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Df 9500 GTAAACCTAATGTGCTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 9559
QY 61 TATATTCCTGTGGAATGACCTATGAGTTTTCAGAAATTTCTCAAAATACGTGTTCAAA 120
Df 9560 TATATTCCTGTGGAATGACCTATGAGTTTTCAGAAATTTCTCAAAATACGTGTTCAAA 9619
QY 121 AATTCCTGTTTGGCACTTTGGGACACCTCAGAAACTTATTAACAACCTGTGAATATGA 180
Df 9620 AATTCCTGTTTGGCACTTTGGGACACCTCAGAAACTTATTAACAACCTGTGAATATGA 9679
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QY 241 AAAACACCAACCTCACACTACTGCTATTCATTATCTGCTAGTGAAGCAAAATGCTTTC 300
Df 9740 AAAACACCAACCTCACACTACTGCTATTCATTATCTGCTAGTGAAGCAAAATGCTTTC 9799
QY 301 TGACTATTAATGTGCACATCAATTCATTCACCTGATAGTAATCATGTAGTAAGCCATT 360
Df 9800 TGACTATTAATGTGCACATCAATTCATTCACCTGATAGTAATCATGTAGTAAGCCATT 9859
QY 361 TGCTGTGTTTCTCTTGTGNTGNATATATCAGTAAATATTTTCCAAAGAGCCATGT 420
Df 361 TGCTGTGTTTCTCTTGTGNTGNATATATCAGTAAATATTTTCCAAAGAGCCATGT 4200
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Db 10220 ACAACAGATTCTAAGTAAATCAATTTTCATTAAAGGAGAAAGAAAAAATTTT 10276

RESULT 5

AAF24685

ID AAF24685 standard; DNA; 10474 BP.

XX AAF24685;

AC AAF24685;

XX 20-APR-2001 (first entry)

DT

XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

DE

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

XX chromosome 9q22-9q31; heart disease; hypercholesterolemia;

XX atherosclerosis; cholesterol transport; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

PH 323..7108

FT /*tag= a

FT /product= "defective ABC1 polypeptide"

XX

PN WO200078972-A2.

XX

PD 28-DEC-2000.

XX

PF 16-JUN-2000; 2000WO-US16765.

XX

PR 18-JUN-1999; 99US-0140264.

PR 14-SEP-1999; 99US-0153872.

PR 19-NOV-1999; 99US-0166573.

XX

XX (CVTH-) CV THERAPEUTICS INC.

PA

XX Lawn RM, Wade D, Garvin M;

PI

XX WPI; 2001-137812/14.

XX

XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,

XX useful for the development of agents for the treatment of heart disease

XX and other disorders associated with hypercholesterolemia and

XX atherosclerosis -

XX

XX Disclosure; Page 148-154; 215pp; English.

XX

XX The present sequence encodes a human adenosine triphosphate (ATP)

XX binding cassette protein (ABC) 1 polypeptide, and is isolated from

XX a Tangier disease patient. ABC1 resides in cell membranes and utilises

XX ATP hydrolysis to transport a wide variety of substrates across the

XX plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated

XX mobilisation of intracellular cholesterol stores. ABC1 is defective in

XX Tangier disease, a genetic disorder characterised by abnormal

XX HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome

XX 9q22-9q31. The ABC1 genes and proteins are useful for developing

XX pharmaceutical agents for the treatment of heart disease and other

XX disorders associated with hypercholesterolemia and atherosclerosis. The

XX genes are useful for developing screening assays to screen for compounds

XX that regulate the expression of genes associated with cholesterol

XX transport. The genes and proteins are also useful for are also useful

XX as diagnostic indicators of cardiovascular disease and other disorders

XX associated with hypercholesterolemia.

XX

XX Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;

XX

XX Query Match 99.5%; Score 773; DB 22; Length 10474;

XX Best Local Similarity 100.0%; Pred. No. 1e-164;

XX Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX 1 GTAACCTAATGTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60

XX

Db 9532 GTAACCTAATGTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9591

QY 61 TATATTCCTGTGGAATGTACCTATGTGAGTTTTCAGAAATTTCTCAAAATAGTGTTTCAA 120

Db 9592 TATATTCCTGTGGAATGTACCTATGTGAGTTTTCAGAAATTTCTCAAAATAGTGTTTCAA 9651

QY 121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTTATTACAACACTGTGAATATGA 180

Db 9652 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTTATTACAACACTGTGAATATGA 9711

QY 181 GAAATACAGAAGAAATTAATAAGCCCTCTATACATAAATGCCACACAAATTCATTGTTA 240

Db 9712 GAAATACAGAAGAAATTAATAAGCCCTCTATACATAAATGCCACACAAATTCATTGTTA 9771

QY 241 AAAACACAAACCTCAGCTACTGTATTTCTATCTATCTGTACTGAAAGCAAAATGCTTTG 300

Db 9772 AAAACACAAACCTCAGCTACTGTATTTCTATCTATCTGTACTGAAAGCAAAATGCTTTG 9831

QY 301 TGACTATTAAATGTTTGCACATCATTTCACTGTATAGTATATCTGACTTAAAGCCATT 360

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QY 361 TGCTGTGTTTCTCTCTGTGNTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGT 420

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QY 481 CTAGAATATATCTACTGNAGAAATATGCTCTAATTTCTTTCAAAATGGTGCATCCGCC 540

Db 10012 CTAGAATATATCTACTGNAGAAATATGCTCTAATTTCTTTCAAAATGGTGCATCCGCC 10071

QY 541 TTAAGAAGTTCTATTTCCATAAGGATTTAGCTTGCTTATCCCTCTTATACCTAGATG 600

Db 10072 TTAAGAAGTTCTATTTCCATAAGGATTTAGCTTGCTTATCCCTCTTATACCTAGATG 10131

QY 601 AAGCTGTTTTTGTGCTCTTTTGTTCATCTGCGCCCTCATTTCCAAAGCACTTTACGCTGTCT 660

Db 10132 AAGCTGTTTTTGTGCTCTTTTGTTCATCTGCGCCCTCATTTCCAAAGCACTTTACGCTGTCT 10191

QY 661 GTAATGGGATCTATTTTGCACCTGGAATATCTGAGAAATGCAAACTAGACAAAGTTTC 720

Db 10192 GTAATGGGATCTATTTTGCACCTGGAATATCTGAGAAATGCAAACTAGACAAAGTTTC 10251

QY 721 ACAACAGATTCTTAAAGTAAATCAATTTTCATTAAAGGAGAAAGAAAAAATTTT 777

Db 10252 ACAACAGATTCTTAAAGTAAATCAATTTTCATTAAAGGAGAAAGAAAAAATTTT 10308

RESULT 6

AAF24686

ID AAF24686 standard; DNA; 10474 BP.

XX AAF24686;

AC AAF24686;

XX

XX 20-APR-2001 (first entry)

DT

XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.

DE

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;

XX apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;

XX chromosome 9q22-9q31; heart disease; hypercholesterolemia;

XX atherosclerosis; cholesterol transport; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

PH 323..7108

FT /*tag= a

FT /product= "defective ABC1 polypeptide"

XX

PN WO200078972-A2.
 XX 28-DEC-2000.
 XX 16-JUN-2000; 2000WO-US16765.
 XX 18-JUN-1999; 99US-0140264.
 PR 14-SEP-1999; 99US-0153872.
 PR 19-NOV-1999; 99US-0166573.
 XX (CVTH-) CV THERAPEUTICS INC.
 PA Lawn RM, Wade D, Garvin M;
 PI WPI: 2001-137812/14.
 XX Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
 PT useful for the development of agents for the treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis -
 XX Disclosure; Page 170-176; 215pp; English.
 PS The present sequence encodes a human adenosine triphosphate (ATP)
 XX binding cassette protein (ABC) 1 polypeptide, and is isolated from
 CC a Tangier disease patient. ABC1 resides in cell membranes and utilizes
 CC ATP hydrolysis to transport a wide variety of substrates across the
 CC plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 CC mobilisation of intracellular cholesterol stores. ABC1 is defective in
 CC Tangier disease, a genetic disorder characterised by abnormal
 CC HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 CC 9q22-9q31. The ABC1 genes and proteins are useful for developing
 CC pharmaceutical agents for the treatment of heart disease and other
 CC disorders associated with hypercholesterolemia and atherosclerosis. The
 CC genes are useful for developing screening assays to screen for compounds
 CC that regulate the expression of genes associated with cholesterol
 CC transport. The genes and proteins are also useful for are also useful
 CC as diagnostic indicators of cardiovascular disease and other disorders
 CC associated with hypercholesterolemia.
 XX SQ Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
 Query Match 99.5%; Score 773; DB 22; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 1e-164;
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTAACCTAATGTGGTAGAAATTTTACCAACTCTATCTACTCAATCAACGCAAAATTTCTG 60
 DB 9532 GTAACCTAATGTGGTAGAAATTTTACCAACTCTATCTACTCAATCAACGCAAAATTTCTG 9591
 QY 61 TATATTCCTGTGGGATGACCTATGTAGTTTCAGAAATCTCAAAATACGTGTTCAAA 120
 DB 9592 TATATTCCTGTGGGATGACCTATGTAGTTTCAGAAATCTCAAAATACGTGTTCAAA 9651
 QY 121 AATTTCTGCTTTTGGCATCTTTGGACACCTCAGAAAACCTATTAACAACCTGTGAATATGA 180
 DB 9652 AATTTCTGCTTTTGGCATCTTTGGACACCTCAGAAAACCTATTAACAACCTGTGAATATGA 9711
 QY 181 GAAATACAGAGAAATATAGCCCTCTATACATAAATGCCACGACAATTCATGTTA 240
 DB 9712 GAAATACAGAGAAATATAGCCCTCTATACATAAATGCCACGACAATTCATGTTA 9771
 QY 241 AAAACAACCAACCACTCACACTACTGTATTTTCATTATCTGTACTGAAACCAATGCTTTG 300
 DB 9772 AAAACAACCAACCACTCACACTACTGTATTTTCATTATCTGTACTGAAACCAATGCTTTG 9831
 QY 301 TCACATTAATATGTTGCACATCAATTCATTCATCTATAGTAAATCAATGACATAAGCCATT 360
 DB 9832 TGACATTAATATGTTGCACATCAATTCATTCATCTATAGTAAATCAATGACATAAGCCATT 9891
 QY 361 TGCTGTGTTTCTTCTGTGGTGNATATATCAGTAAATATTTTCCAAAAGAGCCATGT 420
 DB 9892 TGCTGTGTTTCTTCTGTGGTGNATATATCAGTAAATATTTTCCAAAAGAGCCATGT 9951

QY 421 GTCATGTAATACTGAACCCCTTTGATATTGAGACATTAATTTGGACCCCTGGTATTATCTA 480
 DB 9952 GTCATGTAATACTGAACCCCTTTGATATTGAGACATTAATTTGGACCCCTGGTATTATCTA 10011
 QY 481 CTAGAAATATGTAATCTACTGAGAAATATTGCTCTAAATTTCTTTCAAAATGGTGCATCCCC 540
 DB 10012 CTAGAAATATGTAATCTACTGAGAAATATTGCTCTAAATTTCTTTCAAAATGGTGCATCCCC 10071
 QY 541 TTAANAAGTTCTATTTCCATAAGGATTAGCTTGCTTATCCCTTCTTATACCCCTAAGATG 600
 DB 10072 TTAANAAGTTCTATTTCCATAAGGATTAGCTTGCTTATCCCTTCTTATACCCCTAAGATG 10131
 QY 601 AAGCTGTTTTTGTCTCTTTTCATCATGCGCCCTCATTTCCACGACCTTTACGCTCTCT 660
 DB 10132 AAGCTGTTTTTGTCTCTTTTCATCATGCGCCCTCATTTCCACGACCTTTACGCTCTCT 10191
 QY 661 GTAATGGGATCTATTTTGGCACTGGAATATCTGAGAATTCGAAACCTAGACAAAAGTTTC 720
 DB 10192 GTAATGGGATCTATTTTGGCACTGGAATATCTGAGAATTCGAAACCTAGACAAAAGTTTC 10251
 QY 721 ACAACAGATTTCTAAGTTAAATCATTTTCTATTAAGGAAAAAGAAAAAATTTT 777
 DB 10252 ACAACAGATTTCTAAGTTAAATCATTTTCTATTAAGGAAAAAGAAAAAATTTT 10308
 RESULT 7
 ID AAF24707 standard; DNA; 10474 BP.
 XX AAF24707;
 AC AAF24707;
 XX 20-APR-2001 (first entry)
 DT Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
 DE Human; adenosine triphosphate binding cassette protein 1; ABC1;
 KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
 KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
 KW atherosclerosis; cholesterol transport; ss.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 EH CDS 323..7108
 FT /*tag= a
 FT /product= "defective ABC1 polypeptide"
 XX WO200078971-A2.
 PN 28-DEC-2000.
 PD 16-JUN-2000; 2000WO-US16591.
 XX 18-JUN-1999; 99US-0140264.
 PR 14-SEP-1999; 99US-0153872.
 PR 19-NOV-1999; 99US-0166573.
 XX (CVTH-) CV THERAPEUTICS INC.
 PA (UNIW) UNIV WASHINGTON.
 XX Lawn RM, Wade D, Oram JF, Garvin M;
 PI WPI: 2001-137811/14.
 DR P-PSDB; AAB31366.
 XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
 PT polynucleotides and polypeptides, useful for treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis -
 XX Claim 27; Page 144-150; 211pp; English.
 PS XX

QY	1	GTAAACCTTAATGTGGTGAATAATTTTACCAACTCTATACCTCAATCAAGCAAAATTTCTG	60
Db	9532	GTAAACCTTAATGTGGTGAATAATTTTACCAACTCTATACCTCAATCAAGCAAAATTTCTG	9591
QY	61	TATATTCCCTGTGGAAATGACTATGTGAGTTTCAGAAATTCCAAATACGTTGTTCAA	120
Db	9592	TATATTCCCTGTGGAAATGACTATGTGAGTTTCAGAAATTCCAAATACGTTGTTCAA	9651
QY	121	AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAAACACTGTGAAATATGA	180
Db	9652	AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAAACACTGTGAAATATGA	9711
QY	181	GAAATACAGAGAAATAATATAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA	240
Db	9712	GAAATACAGAGAAATAATATAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA	9771
QY	241	AAAAACAACCAACCTCACACTACTGTATTTTCATTATCTGTACTGAAAGCAAAATGCTTTG	300
Db	9772	AAAAACAACCAACCTCACACTACTGTATTTTCATTATCTGTACTGAAAGCAAAATGCTTTG	9831
QY	301	TGACTATTTAAATGTTGCACATCATTCATTCACTGTATAGTAATCATTTGACTAAGCCATT	360
Db	9832	TGACTATTTAAATGTTGCACATCATTCATTCACTGTATAGTAATCATTTGACTAAGCCATT	9891
QY	361	TGCTGTGTTTTCTCTTGTGGTGNATATATACAGTAAAAATATTTTCCAAAGAGCCATGT	420
Db	9892	TGCTGTGTTTTCTCTTGTGGTGNATATATACAGTAAAAATATTTTCCAAAGAGCCATGT	9951
QY	421	GTCAATGAATACTGAACCCCTTGATATTGAGACATTAATTTGGACCTTGGTATTATCTA	480
Db	9952	GTCAATGAATACTGAACCCCTTGATATTGAGACATTAATTTGGACCTTGGTATTATCTA	10011
QY	481	CTAGAATAATGTAATACTGNAGAAATATGTCTTAATCTTTCAAATGGTGATCCCC	540
Db	10012	CTAGAATAATGTAATACTGNAGAAATATGTCTTAATCTTTCAAATGGTGATCCCC	10071
QY	541	TTAAAANGTTCATTTCATAGGATTTAGCTTGCTTATCCCTTCTTATACCCCTAAGATG	600
Db	10072	TTAAAANGTTCATTTCATAGGATTTAGCTTGCTTATCCCTTCTTATACCCCTAAGATG	10131
QY	601	AAGCTGTTTTTGTGCTCTTTGTTCATCATTTGGCCCTCATTCACAGCACTTTACGCTGTCT	660
Db	10132	AAGCTGTTTTTGTGCTCTTTGTTCATCATTTGGCCCTCATTCACAGCACTTTACGCTGTCT	10191
QY	661	GTAATGGGATCTATTTTTCGACTGGAATATCTGAGAATTGCAAAACCTAGACAAAGTTTC	720
Db	10192	GTAATGGGATCTATTTTTCGACTGGAATATCTGAGAATTGCAAAACCTAGACAAAGTTTC	10251
QY	721	ACAACAGATTTCTAAGTTAAATCAATTTTCATTAAAGGAAAAAGAAAAAATTTT	777

Query Match	99.5%	Score 773;	DB 22;
Best Local Similarity	100.0%	Pred. No. 1e-164;	
Matches 777; Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;			

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
 Db 9532 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 9591
 QY 61 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 120
 Db 9592 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 9651
 QY 121 AATTTCTGCTTTTCGATCTTTGGACACCTCAGAAACTTATTAAACACCTGGAATGA 180
 Db 9652 AATTTCTGCTTTTCGATCTTTGGACACCTCAGAAACTTATTAAACACCTGGAATGA 9711
 QY 181 GAAATACAGAGAAATAAATAAGCCCTCTATACATAATGCCAGACAAATTCATTGTGA 240
 Db 9712 GAAATACAGAGAAATAAATAAGCCCTCTATACATAATGCCAGACAAATTCATTGTGA 9771
 QY 241 AAAACACCAACCTCACACTACTGTATTTTCAATTAATCTGTACTGAAAGCAATGCTTTG 300
 Db 9772 AAAACACCAACCTCACACTACTGTATTTTCAATTAATCTGTACTGAAAGCAATGCTTTG 9831
 QY 301 TGACTATTAATGTGGACATCTTCAATTCACCTGTATAGTAATCACTGAAAGCAATGCTTTG 360
 Db 9832 TGACTATTAATGTGGACATCTTCAATTCACCTGTATAGTAATCACTGAAAGCAATGCTTTG 9891
 QY 361 TGCTGTGTTTCTCTTTGCTGCTGATATATACAGGTAATATTTTCCAAAGAGCCATGT 420
 Db 9892 TGCTGTGTTTCTCTTTGCTGCTGATATATACAGGTAATATTTTCCAAAGAGCCATGT 9951
 QY 421 GTCAATGAATACTGAACCTTTTGATTTGAGACATTAATTTGACCTTGGTATTATCTA 480
 Db 9952 GTCAATGAATACTGAACCTTTTGATTTGAGACATTAATTTGACCTTGGTATTATCTA 10011
 QY 481 CTAGATTAATGTAACTAGAGAAATATTTCTCTAATTTCTTTTCAAAATGCTGATCCCC 540
 Db 10012 CTAGATTAATGTAACTAGAGAAATATTTCTCTAATTTCTTTTCAAAATGCTGATCCCC 10071
 QY 541 TTAAGAGTTCTATTTCATTAAGATTTAGCTGCTTATCCCTTCTATACCTTAAGATG 600
 Db 10072 TTAAGAGTTCTATTTCATTAAGATTTAGCTGCTTATCCCTTCTATACCTTAAGATG 10131
 QY 601 AAGCTGTTTTGCTGCTTTTGTTCATCATTTGGCCCTCATTTCCAAAGACATTTAGCTGTCT 660
 Db 10132 AAGCTGTTTTGCTGCTTTTGTTCATCATTTGGCCCTCATTTCCAAAGACATTTAGCTGTCT 10191
 QY 661 GATATGGATCTATTTTGGACCTGGATATCTGAGAAATTCGAAATAGCAAAAGTTTC 720
 Db 10192 GATATGGATCTATTTTGGACCTGGATATCTGAGAAATTCGAAATAGCAAAAGTTTC 10251
 QY 721 ACAACAGATTCTTAAGTTAAATCATTTTCAATTAAGAGGAAAGGAAAGGAAATTTT 777
 Db 10252 ACAACAGATTCTTAAGTTAAATCATTTTCAATTAAGAGGAAAGGAAAGGAAATTTT 10308

RESULT 9
 ID AAF92831
 XX AAF92831 standard; DNA; 183999 BP.
 AC AAF92831;
 XX AAF92831;

DT 17-MAY-2001 (first entry)
 XX Human ABC1 genomic DNA.
 DE High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ds.
 KW Homo sapiens.
 XX Homo sapiens.
 PN WO200115676-A2.
 XX 08-MAR-2001.
 PD 01-SEP-2000; 2000WO-1B01492.
 PF 01-SEP-2000; 2000WO-1B01492.
 XX

PR 01-SEP-1999; 99US-0151977.
 PR 15-MAR-2000; 2000US-0526193.
 PR 23-JUN-2000; 2000US-0213958.
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON GENETICS INC.
 XX Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
 PI WPI: 2001-244356/25.
 XX
 XX Treating a lower than normal high density lipoprotein-cholesterol
 PT (HDL-C) level, a higher than normal triglyceride level, or a
 PT cardiovascular disease, by administering a compound that modulates LXR-
 PT or RXR-mediated transcriptional activity.
 XX
 XX Claim 8; Fig 1; 317pp; English.
 PS
 XX The present invention relates to a method for treating a patient
 CC diagnosed as having a lower than normal high density
 CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
 CC triglyceride level, or a cardiovascular disease, involving
 CC administering a compound that modulates LXR- or RXR-mediated
 CC transcriptional activity or ABC1 expression or activity.
 CC The LXR gene product may be used in an assay to identify
 CC compounds useful for the treatment of a disease or condition selected a
 CC lower than normal HDL cholesterol level, a higher than normal
 CC triglyceride level, and a cardiovascular disease.
 XX

Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
 Query Match 86.6%; Score 673; DB 22; Length 183999;
 Best Local Similarity 95.7%; Pred. No. 5.8e-142;
 Matches 753; Conservative 10; Mismatches 14; Indels 10; Gaps 7;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
 Db 175214 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 175273
 QY 61 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 120
 Db 175274 TATATCCCTGGAATGTACCTAGTGGAGTTTCAGAAATTCAGAAATTCAGTGTTCAAA 175333
 QY 121 AATTTCTGCTTTTCGATCTTTGGACACCTCAGAAACTTATTAAACACCTGGAATGA 180
 Db 175334 AATTTCTGCTTTTCGATCTTTGGACACCTCAGAAACTTATTAAACACCTGGAATGA 175393
 QY 181 GAAATACAGAGAAATAAATAAGCCCTCTATACATAATGCCAGACAAATTCATTGTGA 240
 Db 175394 GAAATACAGAGAAATAAATAAGCCCTCTATACATAATGCCAGACAAATTCATTGTGA 175453
 QY 241 AAAACACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGAAAGCAATGCTTTG 300
 Db 175454 AAAACACCAACCTCACACTACTGTATTTCAATTAATCTGTACTGAAAGCAATGCTTTG 175513
 QY 301 TGACTATTAATGTGGACATCTTCAATTCACCTGTATAGTAATCACTGAAAGCAATGCTTTG 360
 Db 175514 TGACTATTAATGTGGACATCTTCAATTCACCTGTATAGTAATCACTGAAAGCAATGCTTTG 175573
 QY 361 TGCTGTGTTTCTCTTTGCTGCTGATATATACAGGTAATATTTTCCAAAGAGCCATG 419
 Db 175574 TGCTGTGTTTCTCTTTGCTGCTGATATATACAGGTAATATTTTCCAAAGAGCCATG 175633
 QY 420 TGCTGTGTTTCTCTTTGCTGCTGATATATACAGGTAATATTTTCCAAAGAGCCATG 478
 Db 175634 TGCTGTGTTTCTCTTTGCTGCTGATATATACAGGTAATATTTTCCAAAGAGCCATG 175693
 QY 479 TACTAG-AATAATGTAACTAGNAGAAATATTTGCTTAAATCTTTT-CAAAATGGTGCAT 535
 Db 175694 TACTAGTAAATGTAACTAGNAGAAATATTTGCTTAAATCTTTT-CAAAATGGTGCAT 175753
 QY 536 CCCCCTTAAAG-TTCTATTTCCATAGGATTTAGCT---TGCTTATCCCTTCTTATAC 591
 Db 175753 CCCCCTTAAAG-TTCTATTTCCATAGGATTTAGCT---TGCTTATCCCTTCTTATAC 591

Db 175754 CCCCTTAGATGTTTCTATTTCCATAGAGATTAGGTATGCTATTATCCCTCTTTATAC 175813
Qy 592 CCTAAGATGAGCTGTTTGTGCTGTTGTTGTCATCATATGGCCCTCATTCACAGCACTTT 651
Db 175814 CCTAAGATGAGCTGTTTGTGCTGTTGTTGTCATCATATGGCCCTCATTCACAGCACTTT 175873
Qy 652 ACGCTGCTGTAATGAGATCTATTTTGCACCTGGAATATCTGAG-AATTGCAAAACTAGA 710
Db 175874 ACGCTGCTGTAATGAGATCTATTTTGCACCTGGAATATCTGAGAAATGWAACACTAGA 175933
Qy 711 CAAAGTTTCCACACAGATTCTTAAGTTAAATCAATTTTCAATTAAGGAAAGAAAGAAAA 770
Db 175934 CAAAGTTTCCACACAGATTCTTAAGTTAAATCAATTTTCAATTAAGGAAAGAAAGAAAA 175993
Qy 771 AAATTTT 777
Db 175994 AAATTTT 176000
RESULT 10
ID AAS04049 standard; DNA; 5352 BP.
XX AAS04049;
AC
CC
CT 12-SEP-2001 (first entry)
DT
DE Human ABC1 gene, partial genomic clone #15.
XX
KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Intron 1..194
FT /*tag= a
FT /partial
FT /note= "3', end of intron 48; this sequence is
FT specifically claimed"
FT /number= 48
FT /number= 48
FT /number= 195..3088
FT /*tag= b
FT /number= 49
FT /note= "This sequence is specifically claimed"
FT misc_feature 3089..5352
FT /*tag= c
FT /note= "3', distal sequence"
XX
XX WO200130848-A2.
XX
XX
XX PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-EP10886.
XX
XX PR 26-OCT-1999; 99EP-0402668.
XX PR 01-MAR-2000; 2000US-0186260.
XX
XX PA (AVET) AVENTIS PHARMA SA.
XX
XX PI Denefle P, Rosier-Montus M, Arnould-Reguigne I, Prades C, Naudin L;
XX PI Lencine C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB,
XX PI Dean M;
XX
XX DR WPI; 2001-316327/33.
XX
XX PT New human ABC1 nucleic acids and polypeptides for treating
XX PT atherosclerosis, malaria and diabetes -
XX
XX PS Claim 1; Page 179-182; 368pp; English.
XX
XX CC The sequence represents the nucleic acid sequence of human ABC1 gene,

CC partial genomic clone #15, comprising part of intron 48, exon 49,
CC and 3' distal sequence. The nucleic acid sequence, primers and probes
CC derived from the sequence, and polypeptides and vectors are useful for
CC the prevention of atherosclerosis, in a subject affected by a dysfunction
CC in the reverse transport of cholesterol. The polypeptide encoded by the
CC ABC1 gene is useful for screening for an active ingredient for the
CC prevention or treatment of a disease resulting from dysfunction in the
CC reverse transport of cholesterol. The nucleic acids and polypeptides are
CC also useful for treating and preventing cardiovascular and neurological
CC pathologies, and other diseases e.g. Tangier disease, lecithin-
CC cholesterol (LCAT) deficiency, malaria and diabetes.
XX
SQ Sequence 5352 BP; 1675 A; 928 C; 976 G; 1772 T; 1 other;

Query Match 85.7%; Score 666; DB 22; Length 5352;
Best Local Similarity 96.8%; Pred. No. 1.2e-140;
Matches 763; Conservative 0; Mismatches 14; Indels 11; Gaps 8;
QY 1 GTAAACCTAATTTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60
DB 2758 GTAAACCTAATTTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 2817
QY 61 TATATCCCTGCTGGAATGTACCTATGTGAGTTTCAGAAATTTCAAAATACGTGTTCAA 120
DB 2818 TATATCCCTGCTGGAATGTACCTATGTGAGTTTCAGAAATTTCAAAATACGTGTTCAA 2877
QY 121 AATTTCCTCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACCTGTGAATATGA 180
DB 2878 AATTTCCTCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACCTGTGAATATGA 2937
QY 181 GAAATCAGAGAAATAATAAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 240
DB 2938 GAAATCAGAGAAATAATAAAGCCCTCTATACATAAATGCCAGCACAAATTCATTGTTA 2997
QY 241 AAAACAACCAACCTCAGACACTACTGTATTTTCAATTTTCTACTGAAAGCAAAATGTTT 300
DB 2998 AAAACAACCAACCTCAGACACTACTGTATTTTCAATTTTCTACTGAAAGCAAAATGTTT 3057
QY 301 TGACTATTAATGTTGCACATCATTCATTCACCTGTATAGTAATCAATGACTAAAGCCATT 360
DB 3058 TGACTATTAATGTTGCACATCATTCATTCACCTGTATAGTAATCAATGACTAAAGCCATT 3117
QY 361 TG-CTGTGTTTCTCTTGTGGTGNATATATCAGTAAATATTTTCCAAAGGCCATG 419
DB 3118 TGCTGTGTTTCTCTTGTGGTGNATATATCAGTAAATATTTTCCAAAGGCCATG 3177
QY 420 TGTCATCTAATCTGAACACC-CTTTGATATTGAGACATTAATTTGGACCCCT-TGCTATTAT 477
DB 3178 TGTCATCTAATCTGAACACCCTTTGATATTGAGACATTAATTTGGACCCCTGTATTAT 3237
QY 478 CTACTAG-AATAATGTAATCTAGAGAAATATTCCTCTAATTCCTT--CAAAATGGTGA 534
DB 3238 CTACTAGTAATGTAATCTAGAGAAATATTCCTCTAATTCCTT--CAAAATGGTGA 3297
QY 535 TCCCCCTTAAAANG-TTCTATTTCCATAAGGATTTAGCT--TGCTTATCCCTCTTATA 590
DB 3298 TCCCCCTTAAAANG-TTCTATTTCCATAAGGATTTAGCT--TGCTTATCCCTCTTATA 3357
QY 591 CCCTAAGATGAAGCTGTTTGTGCTCTTTGTCATCATTTGGCCCTCATTCGAGCACTT 650
DB 3358 CCCTAAGATGAAGCTGTTTGTGCTCTTTGTCATCATTTGGCCCTCATTCGAGCACTT 3417
QY 651 TACGCTCTCTAATGGAATCTATTTTGCACCTGGAATATCTGAGATTCGAAACACTAGA 710
DB 3418 TACGCTCTCTAATGGAATCTATTTTGCACCTGGAATATCTGAGATTCGAAACACTAGA 3477
QY 711 CAAAGTTTCCACACAGA-TTTCCTAAGTTAAATCAATTTTCAATTAAGGAAAGAAAA 769
DB 3478 CAAAGTTTCCACACAGATTTTCTAAGTTAAATCAATTTTCAATTAAGGAAAGAAAA 3537
QY 770 AAATTTT 777
DB 3538 AAATTTT 3545

RESULT 11
AAI93913
ID AAI93913 standard; cDNA; 5097 BP.

XX AC AAI93913;
XX DT 13-NOV-2001 (first entry)
XX DE Human stomach cancer expressed polynucleotide SEQ ID NO 140.

XX KW Human; stomach cancer; marker; screening; micro-metastasis;
XX KW peritoneal dissemination; ss.

XX OS Homo sapiens.
XX PN WO200109317-A1.
XX PD 08-FEB-2001.

XX PF 28-JUL-2000; 2000WO-JP05063.
XX PR 29-JUL-1999; 99JP-0248036.
XX PR 27-AUG-1999; 99JP-0300253.
XX PR 18-OCT-1999; 99US-0159590.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 17-FEB-2000; 2000US-0183322.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani H;
XX PI Kodama T, Midorikawa Y;
XX DR WPI; 2001-570287/64.
XX DR P-PSDB; AAM94035.

XX PT New Stomach cancer-associated genes, useful as markers in blood tests
XX PT for screening for the early stages of the disease
XX PS Claim 1; Page 224-226; 242pp; Japanese.

XX CC The invention relates to stomach cancer-expressed genes
XX CC (AAI93842-AAI93917) and the encoded proteins (AAM93967-AAM94039). The
XX CC genes can be used as markers in blood tests for screening for the early
XX CC stages of the disease. The proteins and peptides can be used as targets
XX CC for screening for compounds to treat the disease. They can also be used
XX CC for predicting micro-metastases. The gene can predict peritoneal
XX CC dissemination.

XX SQ Sequence 5097 BP; 1495 A; 991 C; 1010 G; 1601 T; 0 other;
Query Match. 85.5%; Score 664.2; DB 22; Length 5097;
Best Local Similarity 96.6%; Pred. No. 2.9e-140;
Matches 741; Conservative 0; Mismatches 17; Indels 9; Gaps 6;

QY 1 GTAACTAATTCGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTCGTG 60
Db 4331 GTAACTAATTCGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTCGTG 4390

QY 61 TATATCCCTGTTGATGATGACCTATGAGTTTCAGAAATTCCTCAAAATACGTGTCAA 120
Db 4391 TATATCCCTGTTGATGATGACCTATGAGTTTCAGAAATTCCTCAAAATACGTGTCAA 4450

QY 121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTATTAACTGTGAATATCA 180
Db 4451 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAACCTATTAACTGTGAATATCA 4510

QY 181 GAAATACAGAGAAATAATAATAGCCCTCTATACATAAATGCCAGCAAAATTCATTGTTA 240
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Db 4511 GAAATACAGAGAAATAATAATAGCCCTCTATACATAAATGCCAGCAAAATTCATTGTTA 4570
QY 241 AAAACAACCAACCTCACACTACTGTAATTCATTATCTGTACTGTAAGCAAAATGCTTTG 300
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Db 4571 AAAACAACCAACCTCACACTACTGTAATTCATTATCTGTACTGTAAGCAAAATGCTTTG 4630
QY 301 TGAATTAATGTTGACATCATTCATTCACCTGATAGTAATCAATGACTAAAGCCATT 360
|||||
Db 4631 TGAATTAATGTTGACATCATTCATTCACCTGATAGTAATCAATGACTAAAGCCATT 4690
QY 361 T-GCTGTGTTTCTTCTTGTGGTGNATATATCAGGTAATAATATTTCCAAAGAGCCATTG 419
|||||
Db 4691 TATCTGTGTTTCTTCTTGTGGTGNATATATCAGGTAATAATATTTCCAAAGAGCCATTG 4750
QY 420 TGTCAATGTAATCTGAACC-CTTTGATATGAGACATTAATTTGGACCTTTGGTATTATC 478
|||||
Db 4751 TGTCAATGTAATCTGAACCCTTTGATATGAGACATTAATTTGGACCTTTGGTATTATC 4810
QY 479 TACTAG-AATAATGTAATCTGAGAAATATGCTCTAATTCCTT--CAAAATGTTGCTAT 535
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Db 4811 TACTAGTAATGTAATCTGAGAAATATGCTCTAATTCCTT--CAAAATGTTGCTAT 4870
QY 536 CCCCCTTAAAG-TTCTATTTCCATAGGATTTAGCT---TGCTTATCCCTTCTTATATC 591
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Db 4871 CCCCCTTAAAGTCTTCTATTTCCATAGGATTTAGGATGCTATATATCCCTTCTTATATC 4930
QY 592 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCATTTGGCCCTCATTCGAAGCACTTT 651
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Db 4931 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCATTTGGCCCTCATTCGAAGCACTTT 4990
QY 652 AGCTGCTCTGTAATGGGATCTATTTTGCACCTGGAAATATCTCAGAAATGCAAAAGTACAG 711
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Db 4991 AGCTGCTCTGTAATGGGATCTATTTTGCACCTGGAAATATCTCAGAAATGCAAAAGTACAG 5050
QY 712 AAAAGTTTCACAAACAGATTTCTAAGTTAAATCATTTTCAATTTTAAAGG 758
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Db 5051 AAAAGTTTCACAAACAGATTTCTAAGTTAAATCATTTTCAATTTTAAAGG 5097

RESULT 12
AAH18233

ID AAH18233 standard; cDNA; 5097 BP.

XX AC AAH18233;
XX DT 26-JUN-2001 (first entry)
XX DE Human cDNA sequence SEQ ID NO:18170.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX OS Homo sapiens.
XX PN EP1074617-A2.
XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-0116126.
XX PR 29-JUL-1999; 99JP-0248036.
XX PR 27-AUG-1999; 99JP-0300253.
XX PR 11-JAN-2000; 2000JP-0118776.
XX PR 02-MAY-2000; 2000JP-0183767.
XX PR 09-JUN-2000; 2000JP-0241899.

XX PA (HELI-) HELIX RES INST.
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX DR WPI; 2001-318749/34.
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 21.3667 Seconds
(without alignments)
11152.306 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

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- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	42.6	5.5	168575	4	US-09-426-290-1
C 2	39.6	5.1	837	4	US-08-998-416-288
C 3	39.6	5.1	7218	1	US-08-332-463-14
C 4	39	5.0	6265	4	US-09-129-112-3
C 5	38	4.9	1349	2	US-08-676-782-10
C 6	37.8	4.9	1164	3	US-08-794-796-1
C 7	37.8	4.9	5433	3	US-08-929-329-1
C 8	37.2	4.8	6124	4	US-08-213-4198-3
C 9	36.6	4.7	1149	4	US-09-134-001C-2612
C 10	36.6	4.7	1189	1	US-08-307-591-2
C 11	36.2	4.7	1578	4	US-09-044-404A-1
C 12	36.2	4.7	2637	4	US-09-134-001C-1541
C 13	36.2	4.7	21234	4	US-09-810-671-3
C 14	35.6	4.6	1864	4	US-09-468-265-4
C 15	35.4	4.6	912	4	US-09-134-001C-1352
C 16	35.4	4.6	3095	6	5231168-1
C 17	34.8	4.5	610	1	US-08-463-115-50
C 18	34.8	4.5	610	1	US-08-465-388-50
C 19	34.8	4.5	785	4	US-08-936-165A-82
C 20	34.8	4.5	1835	4	US-09-512-342-2
C 21	34.8	4.5	2861	1	US-08-299-953-1
C 22	34.8	4.5	2861	1	US-08-459-415-1
C 23	34.8	4.5	2861	4	US-09-066-687-1
C 24	34.8	4.5	2861	5	PCT-US95-11231-1
C 25	34.8	4.5	3861	1	US-08-299-953-2
C 26	34.8	4.5	3861	1	US-08-459-415-2
C 27	34.8	4.5	3861	4	US-09-066-687-2

C 28	34.8	4.5	3881	5	PCT-US95-11231-2
C 29	34.8	4.5	4673	1	US-07-638-431-1
C 30	34.8	4.5	4673	5	PCT-US92-00018-1
C 31	34.6	4.5	789	6	5219739-8
C 32	34.6	4.5	1001	4	US-09-641-638-465
C 33	34.6	4.5	1001	4	US-09-641-638-466
C 34	34.6	4.5	1002	4	US-09-641-638-595
C 35	34.6	4.5	1101	4	US-09-134-001C-2665
C 36	34.4	4.4	1864	4	US-09-468-265-4
C 37	34.4	4.4	2875	3	US-08-714-918-8
C 38	34.4	4.4	2875	4	US-09-265-315-8
C 39	34.4	4.4	2875	4	US-09-265-315-8
C 40	34.4	4.4	2875	4	US-09-266-417-8
C 41	34.2	4.4	2360	1	US-08-039-364-1
C 42	34.2	4.4	2360	4	US-09-158-710-1
C 43	34.2	4.4	3095	6	5231168-1
C 44	34.2	4.4	19124	2	US-08-487-826B-13
C 45	34	4.4	874	3	US-09-020-033-2

ALIGNMENTS

RESULT 1

US-09-426-290-1/c
; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345, 2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 168575
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21181)...(21403)
; NAME/KEY: CDS
; LOCATION: (95252)...(95430)
; NAME/KEY: CDS
; LOCATION: (101753)...(101996)
; NAME/KEY: CDS
; LOCATION: (110324)...(110439)
; NAME/KEY: CDS
; LOCATION: (124058)...(124278)
; NAME/KEY: CDS
; LOCATION: (127009)...(127130)
; NAME/KEY: CDS
; LOCATION: (128910)...(129139)
; US-09-426-290-1

Query Match 5.5%; Score 42.6; DB 4; Length 168575;
Best Local Similarity 47.3%; Pred. No. 0.46;
Matches 129; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

QY	55	TTTCTGTATATTCCTCGTGGAAATGACCTATCTTTGGACACCTTCAGAAATCTTCAAAATACGTCG 114
DB	14989	TTTCAATTTTCCAGCTGTGCTCTTACTATGATAGTTTAAATCTTAAACAAGACATTT 14930
QY	115	TTCAAAATTTCTGCTTTTCATCTTTGGACACCTTCAGAAATCTTCAAAATACGTCG 174
DB	14929	GTAATATATTAATTTTACATATTTAAAAAATCCAGTGTGTTTAAACAGTACTGA 14870
QY	175	ATATGAAATACAGAGAAATTAATAAGCCCTCTATACATAATGCCACGACATTTCA 234
DB	14869	AAAGTAGAATTATAGGGAACTTGTATATCTTTCAGGATGACATCTCCCCCAAGAGAA 14810

QY	356	CCATTTCGCTGTTTCTTCTTCTTGGTGNATATATACAGGTAAATAATTTTCCAAAGAGC	415
Db	1137	YY	1196
QY	416	CAGTGTGCATGTAATCTGAACCCCTTGCATATGAGACATTAATTTGGACCCCTGGTATT	475
Db	1197	YY	1256
QY	476	ATCTACTAGATAATGTAATCTGACGAGAAATATGCTCTAAATCTTTCAAATGGTGCAT	535
Db	1257	YY	1316
QY	536	CCCCCTTAAANCTTCTATTTCCTCAAGGATTTAGCTGCTTATCCCTTCTATACCCCTA	595
Db	1317	YY	1376
QY	596	AGATGAAGCTGTTTGTGCTCTTTGTTCATCATGCGCCCTCATCCAAAGCAGCTTTACGC	655
Db	1377	YY	1436
QY	656	TGCTCTGAATGGATCTATTTTTCGACTGGAATATCTCAGAAAT	699
Db	1437	ACCAATTTCTTCTATCTCTTTAACTTCTGCTGATAGAGTAAT	1480
RESULT 4			
US-09-129-112-3/C			
; Sequence 3, Application US/09129112			
; Patent No. 6465716			
; GENERAL INFORMATION:			
; APPLICANT: Etzler, Marilyn E.			
; APPLICANT: Murphy, Judith B.			
; APPLICANT: The Regents of the University of California			
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Root			
; FILE REFERENCE: 023070-079810US			
; CURRENT APPLICATION NUMBER: US/09/129,112			
; CURRENT FILING DATE: 1998-08-04			
; PRIOR APPLICATION NUMBER: US 08/907,226			
; PRIOR FILING DATE: 1997-08-06			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: Patentin Ver. 2.1			
; SEQ ID NO 3			
; LENGTH: 6265			
; TYPE: DNA			
; ORGANISM: Dolichos biflorus			
; FEATURE:			
; OTHER INFORMATION: genomic sequence of NBP46 (DB46)			
; NAME/KEY: exon			
; LOCATION: (633)..(944)			
; NAME/KEY: intron			
; LOCATION: (945)..(1022)			
; NAME/KEY: exon			
; LOCATION: (1023)..(1151)			
; NAME/KEY: intron			
; LOCATION: (1152)..(1559)			
; NAME/KEY: exon			
; LOCATION: (1560)..(1616)			
; NAME/KEY: intron			
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; NAME/KEY: exon			
; LOCATION: (1698)..(1790)			
US-09-129-112-3			
Query Match 5.0%; Score 39; DB 4; Length 6265;			
Best Local Similarity 46.2%; Pred. No. 1.5;			
Matches 129; Conservative 0; Mismatches 150; Indels 0; Gaps			
QY	62	ATATTCCCTGCGAATGTACCTATGTGAGTTTCAGAAATTTCCAAATACGTTGTCAAAA	121
Db	2939	ATATATTTTATAGTGTTTTACATTTCAAAATAAACATAATGAGATATGAAGTTTACTGAA	2860
QY	122	ATTTCGTCTTTTCATCTTTGGGACACCTTCAGAAAACATTTATTAACAACGTGTAATATGAG	181

Db 2879 CTCTCTTTTTTTTTTTTTTTTTTTATGTGAATAATGTTTTGAAATATTTGCAAAATATTTAAATAGT 2820

Qy 182 AAATACAGAGAAATAAATAAGCCCTCTATACATAAAATGCCAGACACAAATTCATTGTAA 241

Db 2819 GAATATTATAGAAAAATCCAATAATGAAACTCAAAAAATAATTAATTTATAAGTAA 2760

Qy 242 AAACAACCAAACTCACACTACTGTATTTCATTCTGTCTACTGAACCAAAATCGTTTGT 301

Db 2759 GATCACACAAAGTTTGAATAATTAATTTAAACATATATTAAATATTTACCAAAATACATTT 2700

Qy 302 GACTATTAAATGTTGCACATCATTCATTCCACTGTAGT 340

Db 2699 ATCTTAATAATAAAATAAATTTTAATATAAAATATAAT 2661

RESULT 5

US-08-676-782-10

; Sequence 10, Application US/08676782

; Patent No. 5976792

; GENERAL INFORMATION:

; APPLICANT: CHEUNG, Ambrose

; APPLICANT: FISCHETTI, Vincent A.

; TITLE OF INVENTION: REGULATION OF EXOPROTEIN IN

; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/676,782

; FILING DATE: 08-JUL-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/248,505

; FILING DATE: 25-MAY-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: McGowan, Malcolm K.

; REGISTRATION NUMBER: 39,300

; REFERENCE/DOCKET NUMBER: 016921-092

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1349 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-676-782-10

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	Matches 122;	Conservative	0;	Mismatches	144; Indels
					Gaps
					0;
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DB	418	TTTACTGATAAA	TTCTGAAAATGGGTATAAA	TAGTAGAAGAAGTTAACT	TGGAAGAGT 477
QY	384	GNATATATCAGG	TAAATATTTTCCAAAGAGCCAT	TGTCATGTAACTGAACCC	CTTTTG 443
DB	478	TAAGGTTATACAA	AGGAATCTCTTTAGACACACAT	TGGAATATCGAAACATTTAA	TTTGGCCT 537

; Sequence 2612, Application US/09134001C
; Patent NO. 6380370

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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2612
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; PS-09-134-001C-2612

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Db 475 TAAGTTGTGATTTTAAATGGTTTAAACCTTCCATACATATGGTTCGTAATTTCTT 416

QY 510 GCCTAAATCTTTCAAAA 527
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415 GCTCTAATTTGATAATA 398

Dd

RESULT 10
US-08-307-591-2/c
; Sequence 2, Application US/08307591
; Patent No. 5691138
; GENERAL INFORMATION:

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; APPLICANT: Nucleotide sequences which hybridize
;
; TITLE OF INVENTION: specifically with a Campylobacter jejuni genomic nucleic
;
; TITLE OF INVENTION: sequence.
;
; TITLE OF INVENTION: sequence.
;
; NUMBER OF SEQUENCES: 4
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/307.591
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: INFORMATION FOR SEQ ID NO: 2:
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: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1189 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
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; HYPOTHETICAL: NO
;
; ANTI-SENSE: NO
;
; ORIGINAL SOURCE:
; ORGANISM: Campylobacter jejuni
; TYPE: TIME SOURCE.

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US-08-307-591-2


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RESULT 15
US-09-134--001C-1352/c
; Sequence 1352, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCES: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055, 779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1352
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1352

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Best Local Similarity 52.4%;  Pred No.6.5;
Matches 75;  Conservative 0;  Mismatches 58;  Indels 0;  Gaps 0;

QY 265 TGTATTTTCATATTCGTGACTCAAAAGCAAAATGCTTTTGACACTATTAATAATGTTGCACATCAT 324
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Db 632 TGTTCGTCATCTTTTGTAAGTAGAGTGCAAAAGGTGTTCATCAATAGGAGCTGCACATTTTA 573
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 325 TCATTCAGCTGATAGTAAATCAATTCAGCTAAAGCCAAATTCGTGTTTTCTTCCTGTTGGGNG 384
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 572 TCAITTTTCAATTTTCATATGAATAAATAAAATCTTTTTCCCTTTTATGGTCAATTTCAATA 513
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 385 NATATATCAGTAAATAATTTTC 407
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 TATCTAGGCAATTGATTAATTC 490
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Job time : 188.367 secs

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Db	666	TTTTTTTAACTAATAAAGGATTTATTTAAGGATAGCTTATTTCTTAGGATCTAT	607		
QY	528	TGGTGCATCCCCCTAAAAANGTTCTATTTCOCATAAGGATTTAGCTTGCTTTATCCCTTCCT	587		
Db	606	TTATATACCCCTCTTTATATTAAATAAANAATCTTAAGACTTAGTAAATTTTAAATTTAT	547		
QY	588	ATACCCATAAGATGAAGCTGTTTTTGCTCTTTTGTTCATCATGTGCCCTCATTCACAACA	647		
Db	546	ATTTATTAATATTAAAGCTATAGTCCTGCTTTGCGCTAGTTCCTAGAAAAATTAATTATATAT	487		
QY	648	CTTTACGCTGCTGTAAATGGGATCTATTTTTCGACTCGGAATATCTGGAATTCGAAAAC	707		
Db	486	AAATTATAATACCTTTTTTAAATAGGCTATTAGTAAAAAATTAATATATATCTAAGTATATAA	427		
QY	708	AGACAAAAGTTTCACAACAGATTTCTAAGTTAAATCATTTTCATTAAAAAGGAAAAAAGAA	767		
Db	426	AGGCAATTTATCTAGAAAGTTATGTAGATCTAGTTAATATAATTAGATATACTTA	367		
QY	768	AAAAAATTT	775		
Db	366	GAATATTT	359		

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

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(without alignments)
13866.500 Million cell updates/sec

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Perfect score: 777
Sequence: 1 gtaaacctaattgttgtaga.....gaaaaaagaaaaaaatttt 777

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues
Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq.*
4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubna/FCCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	666	85.7	5352	9	US-09-984-827-22
2	494.4	63.6	601	10	US-09-880-107-1422
3	338	43.5	8925	9	US-09-802-640-27
4	331	42.6	2894	9	US-09-984-827-84
5	331	42.6	2894	9	US-09-984-827-85
6	331	42.6	2894	9	US-09-984-827-86
7	331	42.6	2894	9	US-09-984-827-87
8	331	42.6	2894	9	US-09-984-827-88
9	331	42.6	2894	9	US-09-984-827-89
10	331	42.6	2894	9	US-09-984-827-90
11	331	42.6	9741	9	US-09-984-827-1
12	331	42.6	9741	10	US-09-846-456-10
13	331	42.6	9870	9	US-09-984-827-92
14	331	42.6	9870	9	US-09-984-827-93
15	331	42.6	9870	9	US-09-984-827-94
16	331	42.6	9870	9	US-09-984-827-95
17	331	42.6	9870	9	US-09-984-827-96
18	331	42.6	9870	9	US-09-984-827-97
19	331	42.6	9870	9	US-09-984-827-98

ALIGNMENTS

RESULT 1

US-09-984-827-22
Sequence 22, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: BENEFILE, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 5352
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (374)
OTHER INFORMATION: a, t, c or g
US-09-984-827-22

Query Match 85.7%; Score 666; DB 9; Length 5352;
Best Local Similarity 96.8%; Pred. No. 7.5e-145;
Matches 763; Conservative 0; Mismatches 14; Indels 11; Gaps 8;

QY 1 GTAACCTAATTGTGTAGAAATTTTACCACTCTACTCAATCAACGCAAAATTCG 60
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DB 2758 GTAACCTAATTGTGTAGAAATTTTACCACTCTACTCAATCAACGCAAAATTCG 2817
|||||
QY 61 TATATTCCCTGTGGGAATGACCTATGTAGTTTCAGAAATTCACAAATTCGTTCAA 120
|||||
DB 2818 TATATTCCCTGTGGGAATGACCTATGTAGTTTCAGAAATTCACAAATTCGTTCAA 2877
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Sequence 99, Appl
Sequence 100, Appl
Sequence 101, Appl
Sequence 102, Appl
Sequence 103, Appl
Sequence 104, Appl
Sequence 105, Appl
Sequence 106, Appl
Sequence 107, Appl
Sequence 108, Appl
Sequence 109, Appl
Sequence 110, Appl
Sequence 111, Appl
Sequence 112, Appl
Sequence 113, Appl
Sequence 114, Appl
Sequence 115, Appl
Sequence 116, Appl
Sequence 117, Appl
Sequence 118, Appl
Sequence 119, Appl
Sequence 120, Appl
Sequence 121, Appl
Sequence 122, Appl
Sequence 123, Appl
Sequence 124, Appl

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21 331 42.6 9870 9 US-09-984-827-100
22 331 42.6 9870 9 US-09-984-827-101
23 331 42.6 9870 9 US-09-984-827-102
24 331 42.6 9870 9 US-09-984-827-103
25 331 42.6 9870 9 US-09-984-827-104
26 331 42.6 9870 9 US-09-984-827-105
27 331 42.6 9870 9 US-09-984-827-106
28 331 42.6 9870 9 US-09-984-827-107
29 331 42.6 9870 9 US-09-984-827-108
30 331 42.6 9870 9 US-09-984-827-109
31 331 42.6 9870 9 US-09-984-827-110
32 331 42.6 9870 9 US-09-984-827-111
33 331 42.6 9870 9 US-09-984-827-112
34 331 42.6 9870 9 US-09-984-827-113
35 331 42.6 9870 9 US-09-984-827-114
36 331 42.6 9870 9 US-09-984-827-115
37 331 42.6 9870 9 US-09-984-827-116
38 331 42.6 9870 9 US-09-984-827-117
39 331 42.6 9870 9 US-09-984-827-118
40 331 42.6 9870 9 US-09-984-827-119
41 331 42.6 9870 9 US-09-984-827-120
42 331 42.6 9870 9 US-09-984-827-121
43 331 42.6 9870 9 US-09-984-827-122
44 331 42.6 9870 9 US-09-984-827-123
45 331 42.6 9870 9 US-09-984-827-124

QY 121 AATTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACTGTGAATATGA 180
 Db 2878 AATTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACTGTGAATATGA 2937
 QY 181 GAAATCAGAGAAATAATAAGCCCTCTATACATAAATGCCCAGACAAATTCATTTGTTA 240
 Db 2938 GAAATCAGAGAAATAATAAGCCCTCTATACATAAATGCCCAGACAAATTCATTTGTTA 2997
 QY 241 AAAAAACCAACCACTCAGACTACTCTATTTCATTTCTGTCTGTAAGCAAAATGCTTTG 300
 Db 2998 AAAAAACCAACCACTCAGACTACTCTATTTCATTTCTGTCTGTAAGCAAAATGCTTTG 3057
 QY 301 TGACTATTAAATGTTGCACATCAATTCATTCACCTGTATAGTAATATCAATGACTAAAGCCATT 360
 Db 3058 TGACTATTAAATGTTGCACATCAATTCATTCACCTGTATAGTAATATCAATGACTAAAGCCATT 3117
 QY 361 TG-CTGTTTCTTCTTCTGTTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATG 419
 Db 3118 TGCTGTTTCTTCTTCTGTTGGTGNATATATACAGTAAATATTTTCCAAAGAGCCATG 3177
 QY 420 TGTCATCTAATCTGAACC-CTTTGATATTGAGACATTAATTTGGACCCCT-TGGTATTAT 477
 Db 3178 TGTCATCTAATCTGAACCCTTTGATATTGAGACATTAATTTGGACCCCTGTTATTAT 3237
 QY 478 CTACTAG-ATAATGTAATCTAGNAGAAATATGCTCTAATCTTTT-CAAAATGGTGCA 534
 Db 3238 CTACTAGTAATGTAATCTAGNAGAAATATGCTCTAATCTTTTCAAAATGGTTGCA 3297
 QY 535 TCCCCCTTAAANG-TTCTATTTCATAAGGATTAGCT---TGCTTATCCCTCTTATA 590
 Db 3298 TCCCCCTTAGAATGTTCTATTTCCTAAGGATTAGGATGCTATATCCCTCTTATA 3357
 QY 591 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCAATGCGCCCTCAATCCAAAGCACTT 650
 Db 3358 CCTAAGATGAAGCTGTTTGTGCTTTTGTTCATCAATGCGCCCTCAATCCAAAGCACTT 3417
 QY 651 TAGCGTCTGTAAGGATCTATTGTCATCTGGAATATCTGAGAAATGCAAACTAGA 710
 Db 3418 TAGCGTCTGTAAGGATCTATTGTCATCTGGAATATCTGAGAAATGCAAACTAGA 3477
 QY 711 CAAAGTTTCAACACAGA-TTCTAAGTTAAATCAATTTTCAATAAGGAAAGAAAA 769
 Db 3478 CAAAGTTTCAACACAGATTCTAAGTTAAATCAATTTTCAATAAGGAAAGAAAA 3537
 QY 770 AAAAAATTT 777
 Db 3538 AAAAAATTT 3545

RESULT 2
 ; US-09-880-107-1422/c
 ; Sequence 1422, Application US/09880107
 ; Patent No. US20020142981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Horne, Darci T.
 ; APPLICANT: Vockley, Joseph G.
 ; APPLICANT: Scherf, Uwe
 ; APPLICANT: Gene Logic, Inc.
 ; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 ; FILE REFERENCE: 44921-5028-WO
 ; CURRENT APPLICATION NUMBER: US/09/880,107
 ; CURRENT FILING DATE: 2001-06-14
 ; PRIOR APPLICATION NUMBER: US 60/211,379
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: US 60/237,054
 ; PRIOR FILING DATE: 2000-10-02
 ; NUMBER OF SEQ ID NOS: 3950
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 1422
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA521292
 ; US-09-880-107-1422
 ; Query Match 63.6%; Score 494.4; DB 10; Length 601;
 ; Best Local Similarity 96.0%; Pred. No. 1.9e-105;
 ; Matches 570; Conservative 0; Mismatches 15; Indels 9; Gaps 6;
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 ; 189 GAAGAAATATAAGCCCTCTATACATAAATGCCCAGACAAATTCATTTGTTAAAAACAA 248
 ; Db 601 GAAGAAATATAAGCCCTCTATACATAAATGCCCAGACAAATTCATTTGTTAAAAACAA 542
 ; QY 249 CCAACACCTCACACTACTGTATTTCATTTCTGTACTGAAACAAATGCTTTGTGACTATT 308
 ; Db 541 CCAACACCTCACACTACTGTATTTCATTTCTGTACTGAAACAAATGCTTTGTGACTATT 482
 ; QY 309 AAATGTTGCACATCAATTCATTCACCTGTATAGTAATATCAATGACTAAAGCCATTG-CTGTG 367
 ; Db 481 AAATGTTGCACATCAATTCATTCACCTGTATAGTAATATCAATGACTAAAGCCATTGCTGTG 422
 ; QY 368 TTTTCTTCTTCTGTTGGTGNATATATCAGTAAATATTTTCCAAAGAGCCATGTCATGT 427
 ; Db 421 TTTTCTTCTTCTGTTGGTGNATATATCAGTAAATATTTTCCAAAGAGCCATGTCATGT 362
 ; QY 428 AATCTGAACC-CTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTACTAG-A 485
 ; Db 361 AATCTGAACCACCTTTGATATTGAGACATTAATTTGGACCCCTTGGTATTATCTACTAGTA 302
 ; QY 486 ATAATGTAATCTAGNAGAAATATGCTCTAATCTTTT-CAAAATGGTGCAATCCCCCTTA 543
 ; Db 301 ATAATGTAATCTAGNAGAAATATGCTCTAATCTTTTCAAAATGGTGCAATCCCCCTTA 242
 ; QY 544 AAANG-TTCTATTTCATAAGGATTAGCT---TGCTTATCCCTCTCTATACCCCTAAGAT 599
 ; Db 241 GAATGTTTCTATTTCATAAGGATTAGGATGCTATTATCCCTCTCTATACCCCTAAGAT 182
 ; QY 600 GAAGCTGTTTGTGCTCTTTGTCATCAATGCGCCCTCAATCCAAAGCACTTTAGCGTGC 659
 ; Db 181 GAAGCTGTTTGTGCTCTTTGTCATCAATGCGCCCTCAATCCAAAGCACTTTAGCGTGC 122
 ; QY 660 TGTAATGGATCTATTGTCACCTGGAATATCTGAGAAATGCAAACTAGACAAAGTTT 719
 ; Db 121 TGTAATGGATCTATTGTCACCTGGAATATCTGAGAAATGCAAACTAGACAAAGTTT 62
 ; QY 720 CACAACAGATTCTAAGTTAAATCAATTTTCAATAAGGAAAGAAAAA 773
 ; Db 61 CACAACAGATTCTAAGTTAAATCAATTTTCAATAAGGAAAGAAAAA 8
 ;
 ; RESULT 3
 ; US-09-802-640-27
 ; Sequence 27, Application US/09802640
 ; Publication No. US20030036057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Braun, Andreas
 ; APPLICANT: Bonsal Aruna
 ; APPLICANT: Kleya Patrick
 ; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
 ; FILE REFERENCE: 24736-2048
 ; CURRENT APPLICATION NUMBER: US/09/802,640
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 8925
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (5020)...(6162)
 ; OTHER INFORMATION: Nucleotide encoding ATP-binding cassette (ABC1)
 ; OTHER INFORMATION: n= a or g or c or t

US-09-802-640-27

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Query Match 43.5%; Score 338; DB 9; Length 8925;
Best Local Similarity 100.0%; Pred. No. 1.2e-68;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 60
Db 8588 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 8647
QY 61 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 120
Db 8648 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 8707
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 180
Db 8708 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 8767
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 240
Db 8768 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 8827
QY 241 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 300
Db 8828 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 8887
QY 301 TGACTATTAAATGTGACATCATTCATTCACCTGTATA 338
Db 8888 TGACTATTAAATGTGACATCATTCATTCACCTGTATA 8925

RESULT 4
US-09-984-827-84
; Sequence 84, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-84

Query Match 42.6%; Score 331; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 120
Db 2624 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 2683
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 2743
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 240
Db 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 2803
QY 241 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 300
Db 2804 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 2863
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US-09-802-640-27

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Query Match 43.5%; Score 338; DB 9; Length 8925;
Best Local Similarity 100.0%; Pred. No. 1.2e-68;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 60
Db 8588 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 8647
QY 61 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 120
Db 8648 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 8707
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 180
Db 8708 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 8767
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 240
Db 8768 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 8827
QY 241 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 300
Db 8828 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 8887
QY 301 TGACTATTAAATGTGACATCATTCATTCACCTGTATA 338
Db 8888 TGACTATTAAATGTGACATCATTCATTCACCTGTATA 8925

RESULT 4
US-09-984-827-84
; Sequence 84, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-84

Query Match 42.6%; Score 331; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 120
Db 2624 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 2683
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QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 2743
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 240
Db 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 2803
QY 241 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 300
Db 2804 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 2863
QY 301 TGACTATTAAATGTGACATCATTCATTCA 331
Db 2864 TGACTATTAAATGTGACATCATTCATTCA 2894
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RESULT 5

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US-09-984-827-85
; Sequence 85, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-85
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Query Match 42.6%; Score 331; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 60
Db 2564 GTAACCTAATGTGGTAGAAATTTTACCACCTCTATCTCTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 120
Db 2624 TATATCCCTGTGGAATGTACCTATGTAGTTTCAGAAATTCCTCAAAATACGTTTCAAA 2683
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 180
Db 2684 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAATCTTATTAACAACCTGTGAATATGA 2743
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 240
Db 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAATGCCGACACAAATTCATTGTTA 2803
QY 241 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 300
Db 2804 AAAAACAACCAACCTCAGACTACTGTATTTCAATTTCTACTGTACTGAAAGCAAAATGCTTTG 2863
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QY 301 TGACTATTAAATGTCACATCATTCATTCA 331
|||||
Db 2864 TGACTATTAAATGTCACATCATTCATTCA 2894

RESULT 6

US-09-984-827-86
; Sequence 86, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-86

Query Match 42.6%; Score 331; DB 9; Length 2894;

Best Local Similarity 100.0%; Pred. No. 3.le-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
|||||
Db 2564 GTAAACCTAATTTGGTAGAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATCCCTGGGAATGACCTATGTGAGTTTCAGAAATTCAGAAATACGTTTCAA 120
|||||
Db 2624 TATATCCCTGGGAATGACCTATGTGAGTTTCAGAAATTCAGAAATACGTTTCAA 2683
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAACAACCTGTAATATGA 180
|||||
Db 2684 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAACAACCTGTAATATGA 2743
QY 181 GAAATACAGAAGAAATAATAGCCCTCTATACATAAATGCCAGACAAATTCATTGTTA 240
|||||
Db 2744 GAAATACAGAAGAAATAATAGCCCTCTATACATAAATGCCAGACAAATTCATTGTTA 2803
QY 241 AAAAAACACCAACCTCAGACTACTGTATTTCAATTTCTGTACTGAAAGCAAAATGCTTTG 300
|||||
Db 2804 AAAAAACACCAACCTCAGACTACTGTATTTCAATTTCTGTACTGAAAGCAAAATGCTTTG 2863
QY 301 TGACTATTAAATGTCACATCATTCATTCA 331
|||||
Db 2864 TGACTATTAAATGTCACATCATTCATTCA 2894

RESULT 7

US-09-984-827-87
; Sequence 87, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-87

Query Match 42.6%; Score 331; DB 9; Length 2894;

Best Local Similarity 100.0%; Pred. No. 3.le-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
|||||
Db 2564 GTAAACCTAATTTGGTAGAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATCCCTGGGAATGACCTATGTGAGTTTCAGAAATTCAGAAATACGTTTCAA 120
|||||
Db 2624 TATATCCCTGGGAATGACCTATGTGAGTTTCAGAAATTCAGAAATACGTTTCAA 2683
QY 121 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAACAACCTGTAATATGA 180
|||||
Db 2684 AATTTCTGCTTTTGGCATCTTTGGGACACCTCAGAAAACCTTATTAACAACCTGTAATATGA 2743
QY 181 GAAATACAGAAGAAATAATAGCCCTCTATACATAAATGCCAGACAAATTCATTGTTA 240
|||||
Db 2744 GAAATACAGAAGAAATAATAGCCCTCTATACATAAATGCCAGACAAATTCATTGTTA 2803
QY 241 AAAAAACACCAACCTCAGACTACTGTATTTCAATTTCTGTACTGAAAGCAAAATGCTTTG 300
|||||
Db 2804 AAAAAACACCAACCTCAGACTACTGTATTTCAATTTCTGTACTGAAAGCAAAATGCTTTG 2863
QY 301 TGACTATTAAATGTCACATCATTCATTCA 331
|||||
Db 2864 TGACTATTAAATGTCACATCATTCATTCA 2894

RESULT 8

US-09-984-827-88
; Sequence 88, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 88
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-88

Query Match 42.6%; Score 331; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
DB 2564 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTTGTTCAA 120
DB 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTTGTTCAA 2683
QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATGA 180
DB 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATGA 2743
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAATTCATTGTTA 240
DB 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAATTCATTGTTA 2803
QY 241 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
DB 2804 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 2863
QY 301 TGACTATTAAATGTTGCACATCAATTCATCA 331
DB 2864 TGACTATTAAATGTTGCACATCAATTCATCA 2894

RESULT 9
US-09-984-827-89
; Sequence 89, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984, 827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 89
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-89

Query Match 42.6%; Score 331; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
DB 2564 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTTGTTCAA 120
DB 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTTGTTCAA 2683
QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATGA 180
DB 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATGA 2743
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAATTCATTGTTA 240
DB 2744 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGCACAATTCATTGTTA 2803
QY 241 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 300
DB 2804 AAAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAAGCAAAATGCTTTG 2863
QY 301 TGACTATTAAATGTTGCACATCAATTCATCA 331
DB 2864 TGACTATTAAATGTTGCACATCAATTCATCA 2894

RESULT 10
US-09-984-827-90
; Sequence 90, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984, 827
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (180)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-90

Query Match 42.6%; Score 331; DB 9; Length 2894;
Best Local Similarity 100.0%; Pred. No. 3.1e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
DB 2564 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 2623
QY 61 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTTGTTCAA 120
DB 2624 TATATTCCTGTTGGAATGTACCTATGTGAGTTTCAGAAATCTCAAAATACGTTGTTCAA 2683
QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATGA 180
DB 2684 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAACTTATTAAACAATGTAATGA 2743

QY 181 GAAATACAGAGAAATAAATAGCCCTCTATACATAAAATGCCAGACACAATTCATTGTTA 240
Db 2744 CAAATACAGAGAAATAAATAGCCCTCTATACATAAAATGCCAGACACAATTCATTGTTA 2803
QY 241 AAAACACCAACCAACCTCAGACTACTGTATTTTCAATTCATCTGTACTGAAGCAAAATGCTTGG 300
Db 2804 AAAACACCAACCAACCTCAGACTACTGTATTTTCAATTCATCTGTACTGAAGCAAAATGCTTGG 2863
QY 301 TGACTATTAAATGTGCACATCATTCATTCA 331
Db 2864 TGACTATTAAATGTGCACATCATTCATTCA 2894

RESULT 11
US-09-984-827-1
; Sequence 1, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806 0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: modified_base
; LOCATION: (7009)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-1

Query Match 42.6%; Score 331; DB 9; Length 9741;
Best Local Similarity 100.0%; Pred. No. 5,2e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAACCTAATTTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 9393 GTAACCTAATTTGGTAGAAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9452
QY 61 TATATTCCTGCTGGTAGAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 120
Db 9453 TATATTCCTGCTGGTAGAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9512
QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAAACCTTATTAACAACCTGTGAATATGA 180
Db 9513 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAAACCTTATTAACAACCTGTGAATATGA 9572
QY 181 GAAATACAGAGAAATAAATAGCCCTCTATACATAAAATGCCAGACACAATTCATTGTTA 240
Db 9573 GAAATACAGAGAAATAAATAGCCCTCTATACATAAAATGCCAGACACAATTCATTGTTA 2863
QY 241 AAAACACCAACCAACCTCAGACTACTGTATTTTCAATTCATCTGTACTGAAGCAAAATGCTTGG 300
Db 9633 AAAACACCAACCAACCTCAGACTACTGTATTTTCAATTCATCTGTACTGAAGCAAAATGCTTGG 9692
QY 301 TGACTATTAAATGTGCACATCATTCATTCA 331
Db 9693 TGACTATTAAATGTGCACATCATTCATTCA 9723

RESULT 12
US-09-846-456-10
; Sequence 10, Application US/09846456
; Patent No. US20020146792A1
; GENERAL INFORMATION:
; APPLICANT: Rosier, Marie
; APPLICANT: Prades, Catherine
; APPLICANT: Lemoine, Cendrine
; APPLICANT: Naudin, Laurent
; APPLICANT: Deneffe, Patrice
; APPLICANT: Duverger, Nicolas
; APPLICANT: Brewer, Bryan
; APPLICANT: Remaley, Alan
; APPLICANT: Fojo, Silvia
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying
; TITLE OF INVENTION: Activity and Therapeutic Uses
; FILE REFERENCE: 3806.0505
; CURRENT APPLICATION NUMBER: US/09/846,456
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,280
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 9741
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" is chosen from g, a, t and c
US-09-846-456-10

Query Match 42.6%; Score 331; DB 10; Length 9741;
Best Local Similarity 100.0%; Pred. No. 5.2e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTAACCTAATTTGGTAGAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 60
Db 9393 GTAACCTAATTTGGTAGAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9452
QY 61 TATATTCCTGCTGGTAGAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 120
Db 9453 TATATTCCTGCTGGTAGAATTTTACCACTCTATCTCAATCAAGCAAAATTTCTG 9512
QY 121 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAAACCTTATTAACAACCTGTGAATATGA 180
Db 9513 AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAAACCTTATTAACAACCTGTGAATATGA 9572
QY 181 GAAATACAGAGAAATAAATAGCCCTCTATACATAAAATGCCAGACACAATTCATTGTTA 240
Db 9573 GAAATACAGAGAAATAAATAGCCCTCTATACATAAAATGCCAGACACAATTCATTGTTA 2863
QY 241 AAAACACCAACCAACCTCAGACTACTGTATTTTCAATTCATCTGTACTGAAGCAAAATGCTTGG 300
Db 9633 AAAACACCAACCAACCTCAGACTACTGTATTTTCAATTCATCTGTACTGAAGCAAAATGCTTGG 9692
QY 301 TGACTATTAAATGTGCACATCATTCATTCA 331
Db 9693 TGACTATTAAATGTGCACATCATTCATTCA 9723

RESULT 13
US-09-984-827-92
; Sequence 92, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR

```

FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-93

Query Match      42.6%; Score 331; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTAAACCTAATGTGGTAGAAATTTTACCAACTCTATACTCAATCAAGCAAAATTTCTG 60
Ddb                9522 GTAAACCTAATGTGGTAGAAATTTTACCAACTCTATACTCAATCAAGCAAAATTTCTG 9581

61 TATATCCCTGGGAATGTAACCTATGTAGTTCAGAAATTCAGAAATACGTTTCAA 120
Ddb                9582 TATATCCCTGGGAATGTAACCTATGTAGTTCAGAAATTCAGAAATACGTTTCAA 9641

121 AATTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACCTGTGAATGA 180
Ddb                9642 AATTCTGCTTTTGCATCTTTGGGACACCTCAGAAACCTATTAAACAACCTGTGAATGA 9701

181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGACACAAATTCATTGTTA 240
Ddb                9702 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCAGACACAAATTCATTGTTA 9761

241 AAAACAACCAACCTCACACTACGTATTTTATTATCTGTACTGAAAGCAAAATGCTTG 300
Ddb                9762 AAAACAACCAACCTCACACTACGTATTTTATTATCTGTACTGAAAGCAAAATGCTTG 9821

301 TGACTATTAAATGTTGCACATCATTCATTCA 331
Ddb                9822 TGACTATTAAATGTTGCACATCATTCATTCA 9852

RESULT 15
US-09-984-827-94
; Sequence 94, Application US/09984827
; Publication No. US20030056234M1
; GENERAL INFORMATION:
; APPLICANT: DENELEE, PATRICE
; APPLICANT: KOSTER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-0000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 94
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-94

Query Match      42.6%; Score 331; DB 9; Length 9870;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTAAACCTAATGTGGTAGAAATTTTACCAACTCTATACTCAATCAAGCAAAATTTCTG 60
Ddb                9522 GTAAACCTAATGTGGTAGAAATTTTACCAACTCTATACTCAATCAAGCAAAATTTCTG 9581

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QY 61 TATATCCCTGTGGAAATGTACCTATGTGAGTTTCAGAAATTCACAAATACGTGTTCAAA 120
Db 9582 TATATTCCTGTGGAAATGTACCTATGTGAGTTTCAGAAATTCACAAATACGTGTTCAAA 9641
QY 121 AATTTCTGCTTTTGGCAATCTTGGGACACCTCAGAAAACTTATTAACTGTGAATATGA 180
Db 9642 AATTTCTGCTTTTGGCAATCTTGGGACACCTCAGAAAACTTATTAACTGTGAATATGA 9701
QY 181 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACGACAAATTCATTGTTA 240
Db 9702 GAAATACAGAAGAAATAATAAGCCCTCTATACATAAATGCCGACGACAAATTCATTGTTA 9761
QY 241 AAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAGCAAAATGCTTTG 300
Db 9762 AAAACAACCAACCTCACACTACTGTATTTCATTATCTGTACTGAAGCAAAATGCTTTG 9821
QY 301 TGACTATTAAATGTGCACATCATTCA 331
Db 9822 TGACTATTAAATGTGCACATCATTCA 9852

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Search completed: April 4, 2003, 06:44:28
Job time : 114.152 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 878.309 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526C-1_COPY_9500_10276

Perfect score: 777

Sequence: 1 gtaaacctaattgtgttaga.....gaaaaaagaaaaaaatttt 777

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_man:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	502.8	64.7	648	12	BG567118
3	498.4	64.1	624	14	BM768930
c 4	494.4	63.6	601	9	AA521292
5	449.8	57.9	919	12	BG400012
6	444.8	57.2	646	10	AW019972

7	442.8	57.0	678	12	BE971402
8	430	55.3	506	14	BM823180
c 9	428.4	55.1	531	14	BQ025022
c 10	425.4	54.7	640	14	BM978608
c 11	419.4	54.0	485	14	BM830709
c 12	411.8	53.0	709	9	AL048433
c 13	411.8	52.9	624	14	BQ026286
c 14	399.4	51.4	499	10	AW130712
c 15	373.8	48.1	500	12	BG573350
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c 18	343.8	44.2	443	10	AW019981
c 19	337.8	43.5	527	9	AI628099
c 20	335.4	43.2	405	9	AA493786
c 21	334	43.0	432	9	AA669024
c 22	333.8	43.0	431	9	AI802228
c 23	331	42.6	486	9	AI707785
c 24	330.2	42.5	613	14	BM780759
c 25	327	42.1	372	9	AA748860
c 26	327	42.1	451	9	AA434152
c 27	322	41.4	542	14	N63586
c 28	319.4	41.1	437	9	AI359714
c 29	310.6	40.0	411	10	AV661400
c 30	296	38.1	381	10	BE222116
c 31	291	37.5	479	10	AW044702
c 32	284	36.6	353	9	AA328447
c 33	280.4	36.1	3065	11	AK019548
c 34	280	36.0	299	9	AA731742
c 35	277	35.6	447	9	AI356194
c 36	274.8	35.4	376	10	AV656040
c 37	274.4	35.3	438	9	AI819556
c 38	268.4	34.5	270	9	AA625082
c 39	265.2	34.1	660	10	AW020383
c 40	263.4	33.9	424	9	AI241822
c 41	261	33.6	679	10	BB305534
c 42	256.2	33.0	658	12	BF703659
c 43	251.2	32.3	546	13	BM243763
c 44	248	31.9	679	10	BE532770
c 45	246.4	31.7	320	9	AA737119

ALIGNMENTS

RESULT 1
BM769397
LOCUS K-EST0052628 S14K402 Homo sapiens cdna clone S14K402-20-F12 5',
DEFINITION mRNA sequence.
ACCESSION BM769397
VERSION BM769397.1 GI:190999012
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 719)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Beon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: F column: 12
High quality sequence stop: 719.

FEATURES
Location/Qualifiers
1..719

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S14K402-20-F12"
 /clone_lib="S14K402"
 /cell_line="K402"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
 Site_2: NotI; The poly (A) RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dm-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library." 1 others

BASE COUNT 222 a 133 c 95 g 268 t
 ORIGIN

Query Match 73.4%; Score 570; DB 14; Length 719;
 Best Local Similarity 96.4%; Pred. No. 5.6e-99;
 Matches 645; Conservative 0; Mismatches 15; Indels 9; Gaps 6;

QY 1 GTAAACCTAATGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
 Db 51 GTAAACCTAATGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 110
 QY 61 TATATTCCTGTGGAATGATACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTCAA 120
 Db 111 TATATTCCTGTGGAATGATACCTATGTAGTTTCAGAAATTTCTCAAAATACGTGTCAA 170
 QY 121 AATTTCTGCTTTTGCACTTTGGGACACCTCAGAAAATTTATTAACACTGTGAATATGA 180
 Db 171 AATTTCTGCTTTTGCACTTTGGGACACCTCAGAAAATTTATTAACACTGTGAATATGA 230
 QY 181 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCCAGCACAAATTCATGTTA 240
 Db 231 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCCAGCACAAATTCATGTTA 290
 QY 241 AAAACACCAACCTCACACTACTGATTTTCATTTCTGTTACTGAAACCAATGCTTTG 300
 Db 291 AAAACACCAACCTCACACTACTGATTTTCATTTCTGTTACTGAAACCAATGCTTTG 350
 QY 301 TGACTATTAAATGTGACATCAATTCATCTGATAGTAAATCAATGACCTAAAGCCATT 360
 Db 351 TGACTATTAAATGTGACATCAATTCATCTGATAGTAAATCAATGACCTAAAGCCATT 410
 QY 361 TG-CGTGTTTCTTCTTGTGNTGNATATCATAGTAAATATTTTCCAAAGACCCATG 419
 Db 411 TGTCTGTGTTTCTTCTTGTGNTGNATATCATAGTAAATATTTTCCAAAGACCCATG 470
 QY 420 TGTCTGTGTTTCTTCTTGTGNTGNATATCATAGTAAATATTTTCCAAAGACCCATG 478
 Db 471 TGTCTGTGTTTCTTCTTGTGNTGNATATCATAGTAAATATTTTCCAAAGACCCATG 530
 QY 479 TACTAG-AATAATGTAATCTAGTAAATATTTGCTCTAATTTCTTTT-CAAAATGTGAT 535
 Db 531 TACTAGTAAATGTAATCTAGTAAATATTTGCTCTAATTTCTTTTCAAAATGTGAT 590
 QY 536 CCCCTTTAAAANG-TTCATTTTCCAAAGATTTAGCT---TGCTATTCCTTCTTATAC 591
 Db 591 CCCCTTTAAAANG-TTCATTTTCCAAAGATTTAGCT---TGCTATTCCTTCTTATAC 650
 QY 592 CCTAAGATGAAGCTGTTTTTGTGCTTTTGTTCATCATTTGCCCTCATTCACCAAGCTTT 651
 Db 651 CCTAAGATGAAGCTGTTTTTGTGCTTTTGTTCATCATTTGCCCTCATTCACCAAGCTTT 710

QY 652 AGCGTGCTCT 660
 Db 711 AGCGTGCTCT 719

RESULT 2
 BG567118

LOCUS
 DEFINITION

ACCESSION
 VERSION

KEYWORDS
 SOURCE

ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 648)

AUTHORS
 TITLE

JOURNAL
 COMMENT

BG567118 648 bp mRNA linear EST 10-APR-2001
 602589265F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4723121 5',
 mRNA sequence.

ACCESSION BG567118
 VERSION BG567118.1 GI:13574771

KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 648)
 NIH-MGC http://mgi.nci.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-r@mail.nih.gov

REFERENCE Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.

REFERENCE cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.

REFERENCE Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

REFERENCE High quality sequence stop: 639.
 Location/Qualifiers

1..648
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

/clone="IMAGE:4723121"
 /clone_lib="NIH_MGC_76"

/lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGGCCATTATGGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

BASE COUNT 207 a 120 c 84 g 237 t
 ORIGIN

Query Match 64.7%; Score 502.8; DB 12; Length 648;
 Best Local Similarity 95.9%; Pred. No. 3.5e-86;
 Matches 579; Conservative 0; Mismatches 16; Indels 9; Gaps 6;

QY 1 GTAAACCTAATGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 60
 Db 44 GTAAACCTAATGTGTAGAAATTTTACCACTCTATCTACTCAATCAAGCAAAATTTCTG 103

QY 61 TATATTCCTGTGGAATGTACCTATGTAGTTTCAGAAATTTCAAAATACGTGTCAA 120
 Db 104 TATATTCCTGTGGAATGTACCTATGTAGTTTCAGAAATTTCAAAATACGTGTCAA 163

QY 121 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAATTTTAAACACTGTGAATATGA 180
 Db 164 AATTTCTGCTTTTGCATCTTTGGGACACCTCAGAAAATTTTAAACACTGTGAATATGA 223

QY 181 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCAGCACAAATTCATTTGTTA 240
 Db 224 GAAATACAGAAGAAATATAAGCCCTCTATACATTAATGCCAGCACAAATTCATTTGTTA 283

QY 241 AAAAACAACCAACCTCACACTACTGTATTTCATTTCTACTTGAAGCAAAATCTCTTC 300

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|||||
284 CAAAACACCAACCTCACACTACTGTAATTCATTATCTGTAAGCAAAATGCTTTG 343
QY TGACTATTAATGTTGCATCATCTTCAATTCACCTGATAGTATCATTTGACTAAGCCATT 360
Db TGACTATTAATGTTGCATCATCTTCAATTCACCTGATAGTATCATTTGACTAAGCCATT 403
QY TG-CTGTGTTTCTTCTGTGGTGNATATATATCAGGTAAATATATTTTCCAAAGAGCCATG 419
Db TGCTGTGTTTCTTCTGTGGTGNATATATATCAGGTAAATATATTTTCCAAAGAGCCATG 463
QY TGTCATGTAATGTAAGC-CTTTGATATGAGACATTAATTTGGACCCCTTGATATATC 478
Db TGTCATGTAATGTAAGC-CTTTGATATGAGACATTAATTTGGACCCCTTGATATATC 523
QY TACTAG-AATAAGTATATCTGAGAAATATGCTCTTAATCTTTT--CAAAATGGTGCA 535
Db TACTAGTAAATATGTAATATCTGAGAAATATGCTCTTAATCTTTTCAAAATGGTGCA 583
QY CCCCCTTAAANGT-TCTATTTCCATAAGGATTTAGCT---TGCTATCCCTTCTTATAC 591
Db CCCCCTTAAANGT-TCTATTTCCATAAGGATTTAGCT---TGCTATCCCTTCTTATAC 643
QY CCGTA 595
Db CCGTA 647

RESULT 3
BM768930
LOCUS BM768930
DEFINITION K-EST0051975 S14K402 Homo sapiens cDNA clone S14K402-12-H07 5',
mRNA sequence.
ACCESSION BM768930
VERSION BM768930.1 GI:19098545
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 624)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 12 row: H column: 07
High quality sequence stop: 624.
Location/Qualifiers
1. 624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S14K402-12-H07"
/cclone_lib="S14K402"
/cell_line="K402"
/lab_host="Top10F"
/note="Organ: Stomach; Vector: pTZ18RP1; Site:1; EcoRI;
Site:2; NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of

```

EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 204 a 109 c 81 g 230 t
ORIGIN

Query Match 64.1%; Score 498.4; DB 14; Length 624;
Best Local Similarity 97.2%; Pred. No. 2.5e-85;
Matches 558; Conservative 0; Mismatches 10; Indels 6; Gaps 5;

QY 1 GTAACCTAATTTGGTGTAGAAATTTTACCAACTCTATCTCAATCAACGCAAAATTTCTG 60
Db GTAAACCTAATTTGGTGTAGAAATTTTACCAACTCTATCTCAATCAACGCAAAATTTCTG 110
QY 61 TATATTCCTCTGGGATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGCTGTTCAA 120
Db TATATTCCTCTGGGATGTACCTATGTGAGTTTCAGAAATTCCTCAAAATACGCTGTTCAA 170
QY 121 AATTTCTGTTTTGCACTTTTGGGACACCTCAGAAACCTTATACAACTGTGAATATGA 180
Db AATTTCTGTTTTGCACTTTTGGGACACCTCAGAAACCTTATACAACTGTGAATATGA 230
QY 181 GAATACAGAGAAATATAATAGCCCTCTATACATAATGCCAGCACAAATTCATTGTTA 240
Db GAATACAGAGAAATATAATAGCCCTCTATACATAATGCCAGCACAAATTCATTGTTA 290
QY 241 AAAAACAACCAACCTCACACTACTGTAATTTCAATTTCTGTAAGCAAAATGCTTTG 300
Db AAAAACAACCAACCTCACACTACTGTAATTTCAATTTCTGTAAGCAAAATGCTTTG 350
QY 301 TGACTATTAATGTTGCACATCAATTCACCTGATAGTATCAATTCATTTGACTAAGCCATT 360
Db TGACTATTAATGTTGCACATCAATTCACCTGATAGTATCAATTCATTTGACTAAGCCATT 410
QY 361 TG-CTGTGTTTCTTCTGTGGTGNATATATCAGGTAAATATATTTTCCAAAGAGCCATG 419
Db TGCTGTGTTTCTTCTGTGGTGNATATATCAGGTAAATATATTTTCCAAAGAGCCATG 470
QY 420 TGTCATGTAATGTAAGC-CTTTGATATGAGACATTAATTTGGACCCCTTGATATATC 478
Db TGTCATGTAATGTAAGC-CTTTGATATGAGACATTAATTTGGACCCCTTGATATATC 530
QY 479 TACTAG-AATAAGTATATCTGAGAAATATGCTCTTAATCTTT--CAAAATGGTGCA 535
Db TACTAGTAAATATGTAATATCTGAGAAATATGCTCTTAATCTTTTCAAAATGGTGCA 590
QY CCCCCTTAAANGT-TTCTATTTCCATAAGGATTT 568
Db CCCCCTTAAANGT-TTCTATTTCCATAAGGATTT 624

RESULT 4

AA521292/c

LOCUS

DEFINITION

AA521292

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA521292 601 bp mRNA linear EST 20-AUG-1997
aa79e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:827168 3',
mRNA sequence.

AA521292
AA521292.1 GI:2261835
EST.
human.

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 601)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 485.
 Location/Qualifiers
 1. .601

FEATURES
 source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:827188"
 /clone_lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTT-3', Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
 212 a 81 c 106 g 202 t

BASE COUNT
 ORIGIN

Query Match 63.6%; Score 494.4; DB 9; Length 601;
 Best Local Similarity 96.0%; Pred. No. 1.4e-84;
 Matches 570; Conservative 0; Mismatches 15; Indels 9; Gaps 6;
 QY 189 GAAGAAATATTAAGCCCTCTATACATAAATGCCAGCAATTCATTGTTAAAAACAA 248
 DB 601 GAAGAAATATTAAGCCCTCTATACATAAATGCCAGCAATTCATTGTTAAAAACAA 542
 QY 249 CCAAGCTCACACTACTGATTTATTCATCTGTACTGTAAGCAATGCTTTGTGACTATT 308
 DB 541 CCAAGCTCACACTACTGATTTATTCATCTGTACTGTAAGCAATGCTTTGTGACTATT 482
 QY 309 AAATGTTGCACATCATTCATCTAGTATAGTAATCATTCATGACTAAGCAATTTG-CTGTG 367
 DB 481 AAATGTTGCACATCATTCATCTAGTATAGTAATCATTCATGACTAAGCAATTTGCTGTG 422
 QY 368 TTTCTCTCTGTTGGTGNATATATCAGGTAATAATTTCCAAAGAGCAATGTCATGT 427
 DB 421 TTTCTCTCTGTTGGTGNATATATCAGGTAATAATTTCCAAAGAGCAATGTCATGT 362
 QY 428 AATAGTGAACC-CTTTGATTTAGACATTAATTTGGACCTTGTATATCTAGTAG-A 485
 DB 361 AATAGTGAACCCTTTGATTTAGACATTAATTTGGACCTTGTATATCTAGTAGTA 302
 QY 486 ATAAATGTAATAGTGNAGAAATATGCTCTAATTTCTTTT-CAAAATGGTGCATCCGCCCTTA 543
 DB 301 ATAAATGTAATAGTGNAGAAATATGCTCTAATTTCTTTTCAAAATGGTGCATCCGCCCTTA 242
 QY 544 AAAG-TTCTATTTCATTAAGCAATTTAGCT---TGCATTATCCCTTTATACCCCTAAGAT 599
 DB 241 GAATGTTCTATTTCATTAAGCAATTTAGCTATGCTATTTATCCCTTTATACCCCTAAGAT 182
 QY 600 GAAGCTGTTTTGTGCTCTTTTGTTCATCTGCGCCCTCATTCAGCACTTTAGCTGTC 659
 DB 181 GAAGCTGTTTTGTGCTCTTTTGTTCATCTGCGCCCTCATTCAGCACTTTAGCTGTC 122
 QY 660 TCTAATGGGATCTATTTTGCACCTGAATATCTGGAATTCGAAATTCGAAATTCGAAATTCG 719

Db 121 TGTATGGGATCTATTTTGGCACTGGATATCTGAGAATTCGAAAACATAGACAAAGTTT 62
 QY 720 CACAACAGATTTCTAGTTAAATCATTTTCAUTAAAGGAAAAAGAAAAA 773
 Db 61 CACAACAGATTTCTAGTTAAATCATTTTCAUTAAAGGAAAAAGAAAAA 8
 RESULT 5
 BG400012
 LOCUS
 DEFINITION
 BG400012
 VERSION
 BG400012.1 GI:13293460
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LICM1262 row: h column: 18
 High quality sequence stop: 614.

FEATURES
 source

Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4557761"
 /clone_lib="NIH-MGC-75"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGCGCCGAGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."
 300 a 181 c 144 g 294 t

Query Match 57.9%; Score 449.8; DB 12; Length 919;
 Best Local Similarity 92.8%; Pred. No. 4e-76;
 Matches 526; Conservative 0; Mismatches 31; Indels 10; Gaps 5;
 QY 1 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTACTCAATCAAGCAAAATTTCTG 60
 DB 127 GTAAACCTAATTTGGTAGAAATTTTACCAACTCTACTCAATCAAGCAAAATTTCTG 186
 QY 61 TATATTCCTCTGGAATGTACCTATGTAGTTTCAGAAATTTCTCAAAATACGTTTCAA 120
 DB 187 TATATTCCTCTGGAATGTACCTATGTAGTTTCAGAAATTTCTCAAAATACGTTTCAA 246
 QY 121 AATTTCTGCTTTTGGCATCTTTGGACACCTTCAGAACTTATTAACTGTTGAATGA 180
 DB 247 AATTTCTGCTTTTGGCATCTTTGGACACCTTCAGAACTTATTAACTGTTGAATGA 306
 QY 181 GAAATACAGAGAAAAATTAATAGCCCTCTATACATAAATGCCAGCAATTCATTGTTA 240
 DB 307 GAAATACAGAGAAAAATTAATAGCCCTCTATACATAAATGCCAGCAATTCATTGTTA 366

QY 241 AAAAAACAACCAACCTCACACTACTGATTTTCATTTATCTGTACTGAAAGCAAAATGCTTTG 300
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 Db 367 AAAAAACAACCAACCTCACACTACTGATTTTCATTTATCTGTACTGAAAGCAAAATGCTTTG 425
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 QY 301 TGACTATTAAATGTTGCACATCATTCATTCACCTGTATAGTAATCAATTCATTAAGCCAT 360
 |||||
 Db 426 TGACTATTAAATGTTGCACATCATTCATTCACCTGTATAGTAATCAATTCATTAAGCCAT 485
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 QY 361 TG-CTGTGTTTCTCTGTGGNGNATATA-TCAGGTAAATATATTTCACAGAGCCAT 418
 |||||
 Db 486 TGCTGTGTTTCTCTGTGGNGNATATA-TCAGGTAAATATATTTCACAGAGCCAT 545
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 QY 419 GTGTGATGTAATGTAAGCCCTTTGATATTGACATTAATTTGGACCCCTGG-TATTAT 477
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 Db 546 GTGTGATGTAATGTAAGCCCTTTGATATTGACATTAATTTGGACCCCTGG-TATTAT 605
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 QY 478 CTACTAGATAAATGTAATA-CTGNAGAAATATTCGTCFAATTCCTTCAAAATGGT 531
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 Db 606 CTACTAGATAAATGTAATA-CTGNAGAAATATTCGTCFAATTCCTTCAAAATGGT 665
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 QY 532 GCATCCCTTTAAANGTCTATTTC 558
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 Db 666 CGTCCCTTTAGAAATGTTCTATTTC 692
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RESULT 6
 AW019972 646 bp mRNA linear EST 13-SEP-1999
 LOCUS
 DEFINITION
 IMAGE:2482165 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 COMMENT

Human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 646)
 Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
 and Morton,C.C.
 Isolation of novel and known genes from a human fetal cochlear cDNA
 library using subtractive hybridization and differential screening
 Genomics 23, 42-50 (1994)
 95130111
 Contact: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LHAM6176 row: E column: 14
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers
 1..646
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2482165"
 /clone_lib="Morton Fetal Cochlea"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site:1: EcoRI;
 Site:2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo df. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP

FEATURES
 source

XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTCTTTTCTTTT 3'
 BASE COUNT 207 a 107 c 92 g 225 t 15 others
 ORIGIN

Query Match 57.2%; Score 444.8; DB 10; Length 646;
 Best Local Similarity 88.8%; Pred. No. 3.9e-75;
 Matches 564; Conservative 0; Mismatches 54; Indels 17; Gaps 8;

QY 156 AACTTATTAAACACCTGTGAATATGAGAAATACAGAGAAATAAAGCCCTCTATACAT 215
 |||||
 Db 6 AGCTTATTAAACACCTGTGAATATGAGAAATACAGAGAAATAAAGCCCTCTATACAT 65
 |||||
 QY 216 AATGCCCCAGCAATTCATTGTTAAAAAACAACCAACCTCACACTACTGTATTTCATT 275
 |||||
 Db 66 AATGCCCCAGCAATTCATTGTTAAAAAACAACCAACCTCACACTACTGTATTTCATT 125
 |||||
 QY 276 ATCTGTACTGAAAGCAATTCATTGTTGAGTATTAATGTTGACATCATTCATTCAGTGT 335
 |||||
 Db 126 ATCTGTACTGAAAGCAATTCATTGTTGAGTATTAATGTTGACATCATTCATTCAGTGT 185
 |||||
 QY 336 ATAGTAATCATTCATTAAGCCATTTG-CTGTGTTTCTCTGTTGGTGNATATATACAG 394
 |||||
 Db 186 ATAGTAATCATTCATTAAGCCATTTGCTGTGTTTCTCTGTTGGTGNATATATACAG 245
 |||||
 QY 395 GTAAAAATATTTCCAAAGAGCCATGTCATGTAATCTGTAACACC-CTTTGATATTGAGAC 453
 |||||
 Db 246 GTAAAAATATTTCCAAAGAGCCATGTCATGTAATCTGTAACACCCTTTGATATTGAGAC 305
 |||||
 QY 454 ATTAATTTGACCCCTGTTGTTATCTACTAG-AATATGTAATCTGTAACAGAAATATGCT 512
 |||||
 Db 306 ATTAATTTGACCCCTGTTGTTATCTACTAGTAATGTAATCTGTAACAGAAATATGCT 365
 |||||
 QY 513 CTAAATCTTTCAAAA--TGCTGCATCCCTTAAAAANG-TTCTATTCCATAGGATTTA 569
 |||||
 Db 366 CTAAATCTTTCAAAA--TGCTGCATCCCTTAAAAANG-TTCTATTCCATAGGATTTA 425
 |||||
 QY 570 GCT---TGCTTATCCCTTCTTATACCCCTAGATGAGCTGTTTTGCTCTTTGTTTCAT 626
 |||||
 Db 426 GGTATGCTATATCTCTTATACCCCTAGATGAGCTGTTTTGCTCTTTGTTTCAT 485
 |||||
 QY 627 CATTTGCCCTCATTCACCAAGCATTACGCTGCTGTAATGGGATCTATTTTTCGACTGG- 685
 |||||
 Db 486 CATTTGCCCTCATTCACCAAGCATTACGCTGCTGTAATGGGATCTATTTTTCGACTGG 545
 |||||
 QY 686 ---AATATCTGAGAAATGCAAACTAGACAAAAGTTT---CACACAGATTTCTAGTT 738
 |||||
 Db 546 GAATATNTGAGAAATTTGNAANTTTGCCAAAAGTTTNTCCANNAANTTTTAAAGTT 605
 |||||
 QY 739 AATCATTTTTCATTAAGGAGGAAAAAGAAAAA 773
 |||||
 Db 606 AATATNTTTTNTTAAAAAGGAAAAAANA 640
 |||||

RESULT 7
 BE971402 678 bp mRNA linear EST 04-OCT-2000
 LOCUS
 DEFINITION
 mRNA sequence.
 BE971402
 BE971402.1 GI:10584738
 EST.
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 678)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-femail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arranged by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: WGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LICM776 row: i column: 22
 High quality sequence stop: 598.

FEATURES

Location/Qualifiers

1..678

SOURCE

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3934941"

/clone_lib="NIH_MGC_81"

/lab_host="DH10B (TI phage-resistant)"

/note="Organ: muscle (skeletal); Vector: pDNR-LIB

(Clontech); Site: 1: sfll (ggcgctcgcc); Site 2: sfll

(ggcattatggcc); 5' and 3' adaptors were used in cloning

as follows: 5' adaptor sequence: 5'-CAGGCCATTATGGCC-3'

and 3' adaptor sequence:

5'-ATTCTAGCGCGAGCGGCCGACATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size

1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained

inserts by PCR. This library was enriched for full-length

clones and was constructed by Clontech Laboratories (Palo

Alto, CA)."

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RESULT 8

BM823180

LOCUS

DEFINITION

K-EST0094191 SL4K402s1 Homo sapiens cDNA clone SL4K402s1-9-B09 5',

mRNA sequence.

ACCESSION

BM823180

VERSION

BM823180.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 506)

AUTHORS

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

UNPUBLISHED (2002)

CONTACT: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 9 row: B column: 09

High quality sequence stop: 506.

Location/Qualifiers

1..506

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="SL4K402s1-9-B09"

/clone_lib="SL4K402s1"

/cell_line="K402"

/lab_host="Top10F"

/note="Organ: Stomach; Vector: pTZ19Rpl; Site: 1: EcoRI;

Site 2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then dephosphorylated

with tobacco acid pyrophosphatase (TAP). The dephosphorylated

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library. After analyzing and

sequencing about 2,000 - 3,000 colonies in original cDNA

library, the abundant cDNAs were selected and amplified by

PCR reaction using vector region primer including T7

promoter as 5' primer and N(dt)14 as 3' primer. The PCR

products were used as template for synthesis of

biotinylated single stranded RNA by in vitro transcription

reaction. The synthesized RNA probes were hybridized with

antisense single stranded cDNAs prepared from original

library and incubated with avidin-gel. After removing

DNA-RNA hybrids by centrifuge, the subtracted cDNA

libraries were constructed by transformation of the

remaining DNA into competent cells E. coli Top10F' with

electroporation method."

BASE COUNT

170 a

90 c

68 g

178 t

ORIGIN

Query Match

Best Local Similarity

Matches 452: Conservative

0; Mismatches

2; Indels

2; Gaps

55.3%; Score 430; DB 14; Length 506;

Pred. No. 2,7e-72;

Mismatches 2; Indels 2; Gaps 2;

QY 1 GTAAACCTAATTTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 60
 Db 51 GTAAACCTAATTTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 110
 QY 61 TATATTCCTGTTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 120
 Db 111 TATATTCCTGTTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 170
 QY 121 AATTTCTGTTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 180
 Db 171 AATTTCTGTTGGGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 230
 QY 181 GAAATACAGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 240
 Db 231 GAAATACAGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 290
 QY 241 AAAAACAACCACTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 300
 Db 291 AAAAACAACCACTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 350
 QY 301 TGACTATTAATTTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 360
 Db 351 TGACTATTAATTTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 410
 QY 361 TGCTGTTGTTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 419
 Db 411 TGCTGTTGTTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 470
 QY 420 TGCTGTTGTTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 454
 Db 471 TGCTGTTGTTGAGAAATTTTACCAACTCTATCTCAATCAAGCAAAATTTCTG 506

RESULT 9
 BQ025022/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BQ025022 531 bp mRNA linear EST 27-MAR-2002
 UI-1-BB1p-atq-b-03-0-UI.s1 NCI_CGAP_P16 Homo sapiens cDNA clone
 UI-1-BB1p-atq-b-03-0-UI 3', mRNA sequence.
 BQ025022
 BQ025022.1 GI:19760301
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 531)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Steven Brown
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1. 531
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-1-BB1p-atq-b-03-0-UI"
 /tissue_type="Placenta"
 /dev_stage="Full Term"
 /lab_host="DH10B (Life Technologies)"
 /note="Organ: Placenta; Vector: p773-Pac (Pharmacia) with
 a modified polylinker; Site_1: EcoR I; Site_2: Not I;
 NCI_CGAP_P16 is a subtracted cDNA library constructed
 according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GA, AGGA. For additional information, contact: Bento Soares, bento-soares@uiowa.edu
 TAG_LIB=UI-1-BB1p
 TAG_TISSUE=placenta human full term
 TAG_SEQ=AGGA

BASE COUNT 200 a 76 c 90 g 165 t
 ORIGIN

Query Match 55.1%; Score 428.4; DB 14; Length 531;
 Best Local Similarity 95.5%; Pred. No. 5.4e-72;
 Matches 504; Conservative 0; Mismatches 15; Indels 9; Gaps 6;
 QY 255 CTCACACTACTGTAATTCATTATCTGTAAGCAAAATGCTTTGTAATTAATGCT 314
 Db 531 CTCACACTACTGTAATTCATTATCTGTAAGCAAAATGCTTTGTAATTAATGCT 472
 QY 315 TGCACATCATTCATTACCTGTAATTAATTCATTGTAAGCAAAATGCTTTGTAATTAATGCT 373
 Db 471 TGCACATCATTCATTACCTGTAATTAATTCATTGTAAGCAAAATGCTTTGTAATTAATGCT 412
 QY 374 TCTTGTGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGTCATGTAATGCT 433
 Db 411 TCTTGTGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGTCATGTAATGCT 352
 QY 434 GAACC-CTTTGATATGAGACATTAATTTGGACCTTGGTATTATCTACTAG-AATAATG 491
 Db 351 GAACCCTTTGATATGAGACATTAATTTGGACCTTGGTATTATCTACTAGTAATG 292
 QY 492 TAATCTGNAGAAATATGCTCTAATTCCTTT--CAAAATGGTGCATCCCTTAAAG- 548
 Db 291 TAATCTGNAGAAATATGCTCTAATTCCTTT--CAAAATGGTGCATCCCTTAAAGT 232
 QY 549 TTCTATTTCCATAAGGATTTAGCT--TGCTTATCCTTCTTATACCTCAAGATGAAGCT 605
 Db 231 TTCTATTTCCATAAGGATTTAGCTATGCTATATTCCTTCTTATACCTCAAGATGAAGCT 172
 QY 606 GTTTTGTGCTCTTTGTCATCATTTGGCCCTCATTTCCAAAGCACTTTACGCTGCTCTAAT 665
 Db 171 GTTTTGTGCTCTTTGTCATCATTTGGCCCTCATTTCCAAAGCACTTTACGCTGCTCTAAT 112
 QY 666 GGGATCTATTTGCACTGGAATATCTGCAATTCGCAAACTAGACAAAGTTTCACAAC 725
 Db 111 GGGATCTATTTGCACTGGAATATCTGCAATTCGCAAACTAGACAAAGTTTCACAAC 52
 QY 726 AGATTTCTAAGTTAAATCATTTTTCATTAAGGAAAGAAAAAGAAAAA 773
 Db 51 AGATTTCTAAGTTAAATCATTTTTCATTAAGGAAAGAAAAAGAAAAA 4

RESULT 10
 BQ978608/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE

BQ978608 640 bp mRNA linear EST 21-MAR-2002
 UI-CF-DU1-adq-m-13-0-UI.s1 UI-CF-DU1 Homo sapiens cDNA clone
 UI-CF-DU1-adq-m-13-0-UI 3', mRNA sequence.
 BQ978608.1 GI:19598215
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 640)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 791-806 (1996)
 97044477
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES

source

Location/Qualifiers
 1. .640
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-CF-DUL-adq-m-13-0-UI"
 /clone_lib="UI-CF-DUL"
 /tissue_type="Primary Lung Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-CF-DUL is a normalized cDNA library containing the
 following tissue(s): Primary Lung Epithelial Cells. The
 library was constructed according to Bonaldo, Lennon and
 Soares, Genome Research, 6:791-806, 1996. First strand
 cDNA synthesis was primed with an oligo-dT primer
 containing a Not I site. Double stranded cDNA was ligated
 to an EcoR I adaptor, digested with Not I, and cloned
 directionally into pT73-Pac vector. The oligonucleotide
 used to prime the synthesis of first-strand cDNA contains
 a library tag sequence that is located between the Not I
 site and the (dT)18 tail. The sequence tag for this
 library is GCCTGTAGGC.
 TAG_LIB=UI-CF-DUL
 TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
 TAG_SEQ=GGCTGTAGGC"
 239 a 92 c 98 g 211 t

BASE COUNT
ORIGIN

Query Match 54.7%; Score 425.4; DB 14; Length 640;
 Best Local Similarity 95.4%; Pred. No. 1.9e-71;
 Matches 501; Conservative 0; Mismatches 15; Indels 9; Gaps 6;

QY 262 TACTGATTTTCATTTCTACTGAAGCAATGCTTTGTGACTATTAATTTGTCACAT 321
 |||||
 Db 640 TACTGATTTTCATTTCTACTGAAGCAATGCTTTGTGACTATTAATTTGTCACAT 581
 |||||
 QY 322 CATTCATTCAGTGTATAGTAATCATTTGACTAAAGCAATTTGCTGTTTCTTTCTTGG 380
 |||||
 Db 580 CATTCATTCAGTGTATAGTAATCATTTGACTAAAGCAATTTGCTGTTTCTTTCTTGG 521
 |||||
 QY 381 GNTGNATATACAGTAAATATTTTCCAAAGAGCATGTGTCATGTAATCTGAACC-C 439
 |||||
 Db 520 GTGTATATACAGTAAATATTTTCCAAAGAGCATGTGTCATGTAATCTGAACCAC 461
 |||||
 QY 440 TTGTATTTGAGACATTAATTTGGACCTTGCTATTATCTACTAG-AATAATGTAATCT 498
 |||||
 Db 460 TTGTATTTGAGACATTAATTTGTACCTTGTTATATCTACTAGTAATGTAATCT 401
 |||||
 QY 499 GNAAGAAATTTGCTTAATCTTTT--CAAAATGGTGCAATCCCTTAAAGG-TTCTATT 555
 |||||
 Db 400 GTAGAATATTTGCTTAATCTTTTCAAAATGTTGTCATCCCTTAAAGG-TTCTATT 341
 |||||
 QY 556 TCCATAAGGATTTAGCT---TGCTATCCCTTCTTATACCTTAAGATGAAGCTGTTTTG 612
 |||||
 Db 340 TCCATAAGGATTTAGCTATGCTATTAATCCCTTCTTATACCTTAAGATGAAGCTGTTTTG 281

QY 613 TGCTCTTTGTTTCATTCATTTGGCCCTCATTTCCAAGCACTTTACGCTGTCGTGTAATGGGATCT 672
 |||||
 Db 280 TGCTCTTTGTTTCATTCATTTGGCCCTCATTTCCAAGCACTTTACGCTGTCGTGTAATGGGATCT 221
 |||||
 QY 673 ATTTTTCAGCTGGAATATCTGAGAAATTCGAAAGCTAGACAAAGTTTCACACACAGATTTC 732
 |||||
 Db 220 ATTTTTCAGCTGGAATATCTGAGAAATTCGAAAGCTAGACAAAGTTTCACACACAGATTTC 161
 |||||
 QY 733 TAAGTAAATCATTTTCATTTAAAGGAAAAAGAAAAAATTTT 777
 |||||
 Db 160 TAAGTAAATCATTTTCATTTAAAGGAAAAAGAAAAAATTTT 116
 |||||

RESULT 11

BM830709

LOCUS

DEFINITION K-EST010451 S14K402s1 Homo sapiens cDNA clone S14K402s1-22-D02 5',
 mRNA sequence.

ACCESSION BM830709

VERSION BM830709.1

KEYWORDS GI:19187118

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 485)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genom Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 22 row: D column: 02
 High quality sequence stop: 485.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL

COMMENT

FEATURES

source

1. .485
 /location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S14K402s1-22-D02"
 /clone_lib="S14K402s1"
 /cell_line="K402"
 /lab_host="Top10P"
 /note="Organ: Stomach; Vector: pTZ18RPL; Site_1: EcoRI;
 Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tabacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10P' by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library. After analyzing and
 sequencing about 2,000 ~ 3,000 colonies in original cDNA
 library, the abundant cDNAs were selected and amplified by
 PCR reaction using vector region primer including T7
 promoter as 5' primer and N(dT)14 as 3' primer. The PCR
 products were used as template for synthesis of
 biotinylated single stranded RNA by in vitro transcription
 reaction. The synthesized RNA probes were hybridized with
 antisense single stranded cDNAs prepared from original

library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F⁺ with electroporation method."

BASE COUNT	163 a	86 c	64 g	172 t
ORIGIN				
Query Match		54.0%	Score 419.4;	DB 14; Length 485;
Best Local Similarity		99.1%	Pred. No. 2.9e-70;	
Matches 431; Conservative		0;	Mismatches 3;	Indels 1; Gaps 1;

Query Match	54.0%;	Score 419.4;	DB 14;	Length 485;
Best Local Similarity	99.1%;	Pred. NO. 2.9e-70;		

Qy	1	GTAACCTAATGTGGTAGAAATTTTACCAACTCTATACTCAATCAACAGCAAAATTTCTG	60
Db	51	GTAACCTAATGTGGTAGAAATTTTACCAACTCTATACTCAATCAACAGCAAAATTTCTG	110
Qy	61	TATATCCCTGCTGGAATGTACCTATGTGAGTTTCAGAAATTCAGAAATACGTGTTCAA	120
Db	111	TATATCCCTGCTGGAATGTACCTATGTGAGTTTCAGAAATTCAGAAATACGTGTTCAA	170
Qy	121	AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAAACTTATTAACAACCTGTGATATGA	180
Db	171	AATTTCTGCTTTTGCATCTTTGGACACCTCAGAAAACTTATTAACAACCTGTGATATGA	230
Qy	181	GAATACAGAGAAAAAATAAGGCCCTCTACATAAATGCCAGCACAATTCATTGTTA	240
Db	231	GAATACAGAGAAAAAATAAGGCCCTCTACATAAATGCCAGCACAATTCATTGTTA	290
Qy	241	AAAAACAACCAAACTCACACTACTGTATTTTCATTATCTGACTGAAAGCAAAATGCTTTG	300
Db	291	AAAAACAACCAAACTCACACTACTGTATTTTCATTATCTGACTGAAAGCAAAATGCTTTG	350
Qy	301	TGACTATTAATGTGGACATCATTCTACTGTATAGTAATCATTTGACTTAAAGCCATT	360
Db	351	TGACTATTAATGTGGACATCATTCTACTGTATAGTAATCATTTGACTTAAAGCCATT	410
Qy	361	TG-CTGTGTTTTCTTCTGTGGTGNATATATCAGTAAAAATATTTTCCAAAGAGCCCATG	419
Db	411	TGCTGTGTTTTCTTCTGTGGTGTATATATCAGTAAAAATATTTTCCAAAGAGCCCATG	470
Qy	420	TGTCATGTAATACG	434
Db	471	TGTCATGTAATACG	485

RESULT	12
AL048433/c	
LOCUS	709 bp mRNA linear EST 01-MAR-2000
DEFINITION	DXPZP586I1324_r1 586 (synonym: hutel) Homo sapiens cDNA clone DXFPZB586I1324, mRNA sequence.

AL048433
AL048433.1 GI:4727573
EST.
human
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/bases 1 to 700
REFERENCE

REFERENCE
AUTHORS
Düsterhoef, A., Lauber, J., Mewes, H. W., Gassenhuber, J. and Wiemann, S.
TITLE
EST (Düsterhoef, et al.)
PUBLISHED (1988)

UNPUBLISHED (1933)
Contact: Duesterhoeft A
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing

s1 sequence also available.
This clone (DKFp586II324) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

```

FEATURES
  source
    Berlin- Charlottenburg, GERMANY; Email: clone@rzd.de.
    Location/Qualifiers
      1. .709
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="DKFpZp586I1324"
        /clone_lib="586 (synonym: hutel)"
        /tissue_type="uterus"
        /dev_stage="adult"
        /lab_host="nu108"

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BASE COUNT	252 a	102 c	127 g	225 t	3 others
ORIGIN					

Query Match	53.0%;	Score 411.8;	DB 9;	Length 709;
Best Local Similarity	91.0%;	Pred. NO. 7.3e-69;		

Qy	204	CCCTCTATACATAAATGCCGACGACAAATTCATGTTAAAAACAACAA--CCAAACCTCACAC	261
Db	707	CCCTCTATACNAAATGCCGACGACAAATTCATGTTAAAAACAACCCCAACCTTCACAN	648
Qy	262	TACTGTATTTTCATTAT-CTGTACTGAAAG-CAAAATGCTTTGTGACTATTAATATGTTGCAC	319
Db	647	TACTGTATTTTCATTATCCTGTACTGAAAGCAAAATGCTTTGTGACTATTAATATGTTGCAC	588
Qy	320	ATCATTCAATTCACGTATAGTAATAATCATGTACTAGCAAGCCATTGG-CTGTGTTTTCTTCTTG	378
Db	597	ATCATTCAATTCACGTATAGTAATAATCATGTACTAGCAAGCATTTGCTGTGTTTTCTTCTTG	528
Qy	379	TGGTGNATATATCAGGTAAAAATATTTTCCAAAGAGCCATGTGT-CATGTAATACTGAAC	437
Db	527	TGGTGTATATATCCAGGTAATAATTTTCCAAAGGGCCATGTGTCCCATGTAATACTGACC	468
Qy	438	CCTTGTGATATTGAGACATTAATTTGGACCCCTGTGTATTATCTACT--AGATAATATGTAAT	495
Db	467	ACTTGTGATATTGAGACATTAATTTGTACCCCTGTTATTATCTACTTAGTAATAATGTAAT	408
Qy	496	ACTGNAGAAATATTGCTCTAAATCTTTT--CAAAATGTGTGATCCGCCCTTAAFAANG-TTCT	552
Db	407	ACTGTAGAAAATATTGCTCTAAATCTTTTCAAAAATTTGTGATCCGCCCTTAGAATGTTTCT	348
Qy	553	ATTTCCTAAGGATTTAGCT--TGCTTATCCCTCTCTTATACCTTAGATCAAGCTGTTT	609
Db	347	ATTTCCTAAGGATTTAGGTATGCTATTATCCCTCTTATACCTTAGATCAAGCTGTTT	288
Qy	610	TTGTGCTCTTTGTTTCATCATTTGGCCCTCATCTCCAAGCACTTTAGCGTGTCTTAATGGGA	669
Db	287	TTGTGCTCTTTGTTTCATCATTTGGCCCTCATTTCCAAGCACTTTAGCGTGTCTTAATGGGA	228
Qy	670	TCTATTTTTTGACATGCGATATCTGAGAAATTCGAAACTAGACAAAGTTTTCACACAGAT	729
Db	227	TCTATTTTTTGACATGGAATATCTGAGAAATTCGAAACTAGACAAAGTTTTCACACAGAT	168
Qy	730	TTCAAGTTAAATCATTTTTCATTAAAAAGGAAAAAAGAAAAATTTT	777
Db	167	TTCAAGTTAAATCATTTTTCATTAAAAAGGAAAAAAGAAAAAATTTT	120

RESULT 13
BQ026286/c
LOCUS
DEFINITION
UI-1-BB1p-akp-g-08-0-UI.s2 NC1_CGAP_P16 Homo sapiens cDNA clone
UI-1-BB1p-akp-g-08-0-UI 3', mRNA sequence.
ACCESSION
BQ026286
VERSION
BQ026286.1 GI:19761565
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 624)
AUTHORS
NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
Seq primer: M13 FORWARD
POLYA-ies.

FEATURES
source
1. .624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-1-BB1p-akp-g-08-0-UI"
/clone_lib="NCI CGAP_P16"
/tissue_type="Placenta"
/rev_stage="Full Term"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Placenta; Vector: p7T3-Pac (Pharmacia) with
a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_P16 is a subcloned cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
sequence tags for this library are GA, AGCA. For
additional information, contact: Bento Soares,
bento-soares@iowa.edu
TAG_LIB="UI-1-BB1p"
TAG_TISSUE="placenta human full term"
TAG_SEQ="AGCA"
BASE COUNT 229 a 92 c 96 g 207 t

Query Match 52.9%; Score 411; DB 14; Length 624;
Best Local Similarity 95.5%; Pred. No. 1.1e-68;
Matches 486; Conservative 0; Mismatches 14; Indels 9; Gaps 6;
QY 278 CTGTACTGAAGCAATGCTTGTGACTATTAAATGTTGCACATCATTCATTCACGTGAT 337
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Db 624 CTGTACTGAAGCAATGCTTGTGACTATTAAATGTTGCACATCATTCATTCACGTGAT 565
QY 338 AGTAATCATTTGACTAAAGCCATTGCTGTGTTCTTCTGTTGGTGNATATATCAGGT 396
|||||
Db 564 AGTAATCATTTGACTAAAGCCATTGCTGTGTTCTTCTGTTGGTGNATATATCAGGT 505
QY 397 AAATATTTTCCAAAGAGCCATGTGCTGATTAATCTAGTGAAC-CTTGTATTTGAGACAT 455
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Db 504 AAATATTTTCCAAAGAGCCATGTGCTGATTAATCTAGTGAACCTTTGATATGAGACAT 445
QY 456 TAATTTGGACCTTGGTATTAATCTAGTGAACCTTTGATTAATCTAGTGAACCTTTGAT 514
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Db 444 TAATTTGGACCTTGGTATTAATCTAGTGAACCTTTGATTAATCTAGTGAACCTTTGAT 385
QY 515 AATTCCTTTTCAAATTTGTTGCATCCCTTTAAAG-TTCTATTTCCATPAAGGATTTAG 571
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Db 384 AATTCCTTTTCAAATTTGTTGCATCCCTTTAAAG-TTCTATTTCCATPAAGGATTTAG 325
QY 572 T---TGCCTTATCCCTTATACCTTAAGTGAAGCTGTTTGTGCTTTGTTGTTGTTGTTG 628
|||||
Db 324 TATGCTATTAATCCCTTATACCTTAAGTGAAGCTGTTTGTGCTTTTGTGCTTTTGTGTTG 265
QY 629 TTGGCCCTCATTTCCAAAGCACTTTACGCTCTCTGATGGGATCTATTTTTCGACCTGGAT 688
|||||
Db 264 TTGGCCCTCATTTCCAAAGCACTTTACGCTCTCTGATGGGATCTATTTTTCGACCTGGAT 205

QY 689 ATCTGAGATTCGAAAAGTAGACAAAAGTTTCACAAACAGATTTCCTAAGTTAAATCATTTT 748
|||||
Db 204 ATCTGAGATTCGAAAAGTAGACAAAAGTTTCACAAACAGATTTCCTAAGTTAAATCATTTT 145
QY 749 CATTAAAGGAAAAAGAAAAAATTTT 777
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Db 144 CATTAAAGGAAAAAGAAAAAATTTT 116
RESULT 14
AW130712/c
LOCUS AW130712.1 GI:6132244
DEFINITION mRNA sequence.
ACCESSION AW130712
VERSION AW130712.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 499)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Greg Lennon, Ph.D.
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 428.
FEATURES
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1. .499
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2621966"
/clone_lib="NCI CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
BASE COUNT 195 a 74 c 87 g 143 t
ORIGIN
Query Match 51.4%; Score 399.4; DB 10; Length 499;
Best Local Similarity 95.2%; Pred. No. 1.8e-66;
Matches 475; Conservative 0; Mismatches 15; Indels 9; Gaps 6;
QY 260 ACTACTGTATTTTCATTCCTCTACTGTAAGCAAAATGCTTTGTGACTATTAAATGTTGCAC 319
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Db 499 ACTACTGTATTTTCATTCCTCTACTGTAAGCAAAATGCTTTGTGACTATTAAATGTTGCAC 440
QY 320 ATCATTCATTCACCTGATAGTAATCAATGACTAAAGCCATTG-CTGTGTTTCTTCTTG 378
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Db 439 ATCATTCATTCACCTGATAGTAATCAATGACTAAAGCCATTGCTGTTTCTTCTTG 380
QY 379 TGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGTGCTATGTAATGTAAC 438
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Db 379 TGGTGNATATATCAGGTAAATATTTTCCAAAGAGCCATGTGCTATGTAATGTAAC 320
QY 439 -CTTGTATTTGAGACATTAATTTGGACCCCTTGCTATTCTACTAG-AATAATGTAATA 496
|||||

Db	319	AC	TTTGATATTGAGACATTAATTGTTACCCCTGTTTATTATCTACTAGTAATAATGTAATA	260				
QY	497	CT	GNAGAAATATTGCTCTAATCTTTT--CAAAATGGTGCATCCCTCTAAANG-TTCTA	553				
Db	259	CT	GTAAGAAATATTGCTCTAATCTTTTCAAAATTTGTTGCATCCCTCAAGAAATGTTTCTA	200				
QY	554	TT	TCATAAGGAATTTAGCTG---CTATCCCTTCTTATACCCCTAGATGAAGCTGTTTT	610				
Db	199	TT	TCATAAGGAATTTAGTAGGCTATATACCTCTTATACCCCTAGATGAAGCTGTTTT	140				
QY	611	TG	TCCTTTTGTTCATCATTTGGCCCTCATTCACAGCACITTTAGCTGCTCTGTAAATGGAT	670				
Db	139	TG	TGCTCTTTTTCATCATTTGGCCCTCATTCACAGCACITTTACGCTGCTGTAAATGGAT	80				
QY	671	CT	ATTTTTCGACATGGAATATCTGAGAAATGCAAACTAGACAAAAGTTTCACAACAGATT	730				
Db	79	CT	ATTTTTCGACATGGAATATCTGAGAAATGCAAACTAGACAAAAGTTTCACAACAGATT	20				
QY	731	TC	TAAAGTTAAATCATTTTC	749				
Db	19	TT	TAAAGTTAAATCATTTTC	1				
RESULT	15							
LOCUS	BG573350							
DEFINITION	602595120f1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4724381 5', linear EST 10-APR-2001							
ACCESSION	BG573350							
VERSION	1	GI:13591003						
KEYWORDS	EST.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	1 (bases 1 to 500)							
TITLE	NIH-MGC http://mgs.nci.nih.gov/.							
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)							
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgaaps-remail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI585 row: g column: 06 High quality sequence stop: 500. Location/Qualifiers 1. .500							
FEATURES	source							
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/db_xref="taxon:9606"								
/clone="IMAGE:4724381"								
/clone_lib="NIH_MGC_79"								
/lab_host="DH10B (T1 phage-resistant)"								
/note="Organ: placenta; Vector: pDNR-LTB (Clontech); Site_1: Sfil (ggccattatggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."								
BASE COUNT	150 a	85 c	77 g	188 t				
ORIGIN								

Query Match 48.1%; Score 373.8; DB 12; Length 500;
Best Local Similarity 94.4%; Pred. No. 1.4e-61;

Search completed: April 3, 2003, 16:37:12
Job time : 890.309 secs

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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 13444.6 Seconds
(without alignments)
14684.987 Million cell updates/sec

Title: US-09-595-526c-1_COPY_291_7074

Perfect score: 6784

Sequence: 1 atgctgtgttcctcagct.....agtgaagaagactatgtat 6784

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sv.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
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- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pin.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6784	100.0	10442	6	AX060713 Sequence
2	6784	100.0	10442	6	AX060892 Sequence
3	6784	100.0	10442	9	AF285167 Homo sapi
4	6782.4	100.0	10474	6	AX060719 Sequence
5	6782.4	100.0	10474	6	AX060721 Sequence
6	6782.4	100.0	10474	6	AX060898 Sequence
7	6782.4	100.0	10474	6	AX060900 Sequence
8	6776	99.9	7860	6	AX092594 Sequence
9	6769.6	99.8	6786	6	AB055982 Homo sapi
10	6768	99.8	7260	6	AX253452 Sequence
11	6764.8	99.7	9741	6	AX127830 Sequence
12	6764.8	99.7	9741	6	AX139817 Sequence
13	6764.8	99.7	9741	6	AX351038 Sequence
14	6764.8	99.7	9854	6	AX127831 Sequence
15	6764.8	99.7	9854	6	AX139818 Sequence
16	6750.8	98.9	7862	6	AX135712 Sequence
17	6708	98.9	6880	6	AX253450 Sequence
18	6708	98.9	6880	9	HSA012376
19	6708	98.9	9497	6	AX059973 Sequence
20	6708	98.9	9497	9	AF165281 Homo sapi
21	6694	98.7	9495	6	AX059978 Sequence
22	6589.2	97.1	9593	6	AX059976 Sequence
23	5581	82.3	7878	10	MMAB01
24	4345.6	64.1	7074	5	AF362377 Gallus ga
25	1931.6	28.5	7298	9	AF001945 Homo sapi
26	1931.6	28.5	7709	4	BTU90126
27	1928.8	28.4	7268	10	MMAF000149
28	1926.8	28.4	7323	9	HSAF000148
29	1918.8	28.3	7276	9	HSU88667
30	1904.4	28.1	5097	9	BD012346
31	1904.4	28.1	5097	9	AK027864 Homo sapi
32	1904.4	28.1	5097	23	BD005026
33	1742.2	25.7	6704	9	AF328787
34	1742.2	25.7	7795	6	AX429481 Sequence
35	1735.8	25.6	6027	9	AB055390 Homo sapi
36	1735.8	25.6	6432	6	AX320364 Sequence
37	1735.8	25.6	6522	6	AX202218 Sequence
38	1735.8	25.6	6588	9	AF250238 Homo sapi
39	1735.8	25.6	6768	6	AX320362 Sequence
40	1696	25.0	6607	6	AX080493 Sequence
41	1596	25.0	6607	10	AF287141 Mus muscu
42	1531.6	22.6	5762	6	AX080462 Sequence
43	1465	21.6	5669	6	AX202220 Sequence
44	985	14.5	7305	6	AX235953 Sequence
45	985	14.5	7482	9	AF327657 Homo sapi

ALIGNMENTS

RESULT 1	AX060713	Sequence	10442 bp	DNA	linear	PAT 22-JAN-2001
LOCUS	AX060713	Sequence 1	from Patent WO0078972.			
DEFINITION	AX060713					
ACCESSION	AX060713					
VERSION	AX060713.1	GI:12406103				
KEYWORDS	human.					
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 10442)					
AUTHORS	Lawn,R.M., Wade,D. and Garvin,M.					
TITLE	Regulation with binding cassette transporter protein abcl					
JOURNAL	Patent: WO 0078972-A 1 28-DEC-2000;					

Pred. No. is the number of results predicted by chance to have a

FEATURES		CV THERAPEUTICS, INC. (US)			
source	I. .10442	Location/Qualifiers			
		/organism="Homo sapiens"			
		/db_xref="taxon:9606"			
BASE COUNT	2898 a	2297 c	2408 g	2835 t	4 others
ORIGIN					
Query Match 100.0%; Score 6784; DB 6; Length 10442;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 6784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	ATGGCTGTGGCTCAGCTGAGTGGCTGCTGTGGAAGAACCTCACTTTCAAGAAGA	60		
Db	291	ATGGCTGTGGCTCAGCTGAGTGGCTGCTGTGGAAGAACCTCACTTTCAAGAAGA	350		
QY	61	CAAACTGTACAGTGTACTGGAAGTGGCTGGCCCTCTATTATCTTCCTGATCCTGATC	120		
Db	351	CAAACTGTACAGTGTACTGGAAGTGGCTGGCCCTCTATTATCTTCCTGATCCTGATC	410		
QY	121	TCGTTCGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTCCAAATAAGCC	180		
Db	411	TCGTTCGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTCCAAATAAGCC	470		
QY	181	ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTTATCTGTAATGCCAACAACCC	240		
Db	471	ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTTATCTGTAATGCCAACAACCC	530		
QY	241	TGTTTCGGTACCGACTCCTGGGAGGCTCCCGAGTGTGGAACTTTAACAATAATCC	300		
Db	531	TGTTTCGGTACCGACTCCTGGGAGGCTCCCGAGTGTGGAACTTTAACAATAATCC	590		
QY	301	ATTGTGGCTCGCTGTCTCAGATGCTCGAGGCTTCCTTTATACAGCCAGAAAGACACC	360		
Db	591	ATTGTGGCTCGCTGTCTCAGATGCTCGAGGCTTCCTTTATACAGCCAGAAAGACACC	650		
QY	361	AGCATGAAGACATGGCAAGTCTGAGAACATTCAGACAGATCAAGAAATCCAGCTCA	420		
Db	651	AGCATGAAGACATGGCAAGTCTGAGAACATTCAGACAGATCAAGAAATCCAGCTCA	710		
QY	421	AAGTTGAAGCTTCAAGATTTCCTGGTGGACATGAACCTTCCTGGGTTCCTATATCAC	480		
Db	711	AAGTTGAAGCTTCAAGATTTCCTGGTGGACATGAACCTTCCTGGGTTCCTATATCAC	770		
QY	481	AACCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGGGTGATGTCATTCCTCAC	540		
Db	771	AACCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGGGTGATGTCATTCCTCAC	830		
QY	541	AAGGTATTTTCCAAAGGCTACCAATTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	600		
Db	831	AAGGTATTTTCCAAAGGCTACCAATTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA	890		
QY	601	GAAGAGATGATTCAACTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTACCAAAAGAG	660		
Db	891	GAAGAGATGATTCAACTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTACCAAAAGAG	950		
QY	661	AAACTGGGTGACGAGAGGAGTACTCGTTCCAACTGAGACATCCCTGAAGCCATCTCTG	720		
Db	951	AAACTGGGTGACGAGAGGAGTACTCGTTCCAACTGAGACATCCCTGAAGCCATCTCTG	1010		
QY	721	AGAACACTAAACTCTACATCTCCCTTCCCGACGAGGAGTGGGTGAAGCCACAAAACA	780		
Db	1011	AGAACACTAAACTCTACATCTCCCTTCCCGACGAGGAGTGGGTGAAGCCACAAAACA	1070		
QY	781	TGCTGCAATGCTTGGAGCTCTGCCCAGGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC	840		
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QY	841	ATGCACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	900		
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DEFINITION Sequence 1 from Patent WO0078971.
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VERSION AX060892.1 GI:12406270
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JOURNAL CV THERAPEUTICS, INC. (US)
FEATURES
Location/Qualifiers
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BASE COUNT 2898 a 2297 c 2408 g 2835 t 4 others
ORIGIN

Query Match 100.0%; Score 6784; DB 6; Length 10442;
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Matches 6784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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VERSION   AF285167.1
KEYWORDS  AF285167.1 GI:9755158
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ORGANISM  Homo sapiens
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1 (bases 1 to 10442)
ABCA1 gene expression and apoA-I-mediated cholesterol efflux are regulated by LXR
2 (bases 1 to 10442)
Lawn,R.M., Wade,D.P., Garvin,M.R., Wang,X., Schwartz,K., Porter,J.G., Seilhamer,J.J., Vaughan,A.M. and Oram,J.F.
Direct Submission
Submitted (06-JUL-2000) Discovery Research, CV Therapeutics Inc., 3172 Porter Drive, Palo Alto, CA 94304, USA
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QY	3781	ACCTCAGATGTTACCTTCCGCGAGAGCAACAGCGCGGCTTCCGGGACAAACAGAGC	3840
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QY	3961	GGCTGGAACCTTACACCAACAGTTTGTGCGCTTTTGTGGAAGAGACTCTAAATGCC	4020
Db	4251	GGCTGGAACCTTACACCAACAGTTTGTGCGCTTTTGTGGAAGAGACTCTAAATGCC	4310
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RESULT 4
LOCUS AX060719
DEFINITION Sequence 7 from Patent WO0078972.
ACCESSION AX060719
VERSION AX060719.1 GI:12406108
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10474)
AUTHORS Law, R.M., Wade, D. and Garvin, M.
TITLE Regulation with binding cassette transporter protein abc1
JOURNAL Patent: WO 0078972-A 7/28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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QY 301 ATTGTGGCTCGCCTGTTCTCAGATGCTCGAGGCTTCTTTTATACAGCCAGAAAGACAC 360
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QY	1261	CCCAGATCTGGACCTTCATGGAGAACACCGCAAGAAATGGACCTTGTCCGGATGCTGTTG	1320
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QY	1381	CAAGACATCGTGGCGTTTTTGGCCAAAGCACCCACAGAGATGCCAGTCCAGTAATGTTCT	1440
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QY	1441	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC	1500
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Db	2003	GACAATGTGGAGAGGACAAATAAATCAAGATGGTACTGGGACCTGTCTCTCGAGCT	2062
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Db	2303	TATGAGAAGGAGCAGCGCTGAAAGAGACCATGCGGATCATGGCCCTGGACAACAGCAT	2362
QY	2041	CTCTGGTTTACGTGGTTCAITTAGTAGCTCATTCCTCTCTTGTGAGCGCTGGCCTGCTA	2100
Db	2363	CTCTGGTTTACGTGGTTCAITTAGTAGCTCATTCCTCTCTTGTGAGCGCTGGCCTGCTA	2422
QY	2101	GTGTCATCTCTGAAGTTAGGAACCTGCTGCCCTACACTGATCCACAGCGTGGTTTGTCTC	2160
Db	2423	GTGTCATCTCTGAAGTTAGGAACCTGCTGCCCTACACTGATCCACAGCGTGGTTTGTCTC	2482
QY	2161	TTCTGTCCGTGTTTGTGTGTGTGAACAATCCCTGTGAGTGGTTCCTGTATTAGCACACTCTTC	2220
Db	2483	TTCTGTCCGTGTTTGTGTGTGTGAACAATCCCTGTGAGTGGTTCCTGTATTAGCACACTCTTC	2542
QY	2221	TCCAGAGCCAACTGGCAGCAGCCTGTGGGGGCATCTACTTCACGCTGTACTCGCC	2280
Db	2543	TCCAGAGCCAACTGGCAGCAGCCTGTGGGGGCATCTACTTCACGCTGTACTCGCC	2602
QY	2281	TACGTCTCTGTGTGGCAATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGTGAGC	2340
Db	2603	TACGTCTCTGTGTGGCAATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGTGAGC	2662

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QY	2401	GGCATTGGAGTCAGTGGGACAAACCTGTTTCAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2460
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QY	2521	TACATTGAGCTGTCTTTCCAGGCCAGTACGGAAATTCACAGCCCTGGTATTTTCCTTGC	2580
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QY	2581	ACCAAGTCTCTACTGGTTTGGCGAGGAAGTGTATGAGAAAGACCACCTGTGTCCAAACAG	2640
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QY	3001	AAAGGGCTCTCTGAGAGCACGTGAAGCGGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3060
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ACCESSION	AX060721		
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KEYWORDS	human.		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 10474)		
JOURNAL	Lawn, R.M., Wade, D. and Garvin, M.		
FEATURES	Regulation with binding cassette transporter protein abcl		
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Db 3203 GGAAGAGACATCTGCTCTGAGATGAGCACCATCCGCGAGAACTGGGGGTCTGTCCCCAG 3262
QY 2941 CATAGCTGCTGTTTGACATGCTGACTGTGGAAGAACACATCTGTTCTATGCCCGCTTG 3000
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Db	4643	GTTCGCCAGACCATCATGACCTCTTCCAGATATGGAACTGGCAATGCGAACCCTTCA	4702
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QY	5221	CTACTTTTGTGTATGGGTGGTCAATTCACACCTCTCATGTACCCAGCCTCTTTGTGTTTC	5280
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QY 181 ATGCCCTCTGCAGGAACACTTCTTGGTTCAGGGGATTATCTGTAATGCCAACAAACCC 240
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QY 841 ATGCACAGGAGGAGTGTATGTTCTGACCAATGTGAACACTCCAGCTCTCCACCCCAATC 900
Db 1163 ATGCACAGGAGGAGTGTATGTTCTGACCAATGTGAACACTCCAGCTCTCCACCCCAATC 1222
QY 901 TACCAGGCTGTCTGCTGATTTGTCTGCGGCAATCCCGAGGAGGAGGCTGGAAGATCAAG 960
Db 1223 TACCAGGCTGTCTGCTGATTTGTCTGCGGCAATCCCGAGGAGGAGGCTGGAAGATCAAG 1282
QY 961 TCTCTCAACTGATGAGGACAAACACTTACAAAGCCCTCTTTGGAGCAATGGCAGCTGAG 1020
Db 1283 TCTCTCAACTGATGAGGACAAACACTTACAAAGCCCTCTTTGGAGCAATGGCAGCTGAG 1342
QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1080
Db 1343 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1402
QY 1081 AATTGGAGTCTAGTCTCTTTCCCGATTTATCTGGAAGCTCTGAAGCCGCTGCTGCT 1140
Db 1403 AATTGGAGTCTAGTCTCTTTCCCGATTTATCTGGAAGCTCTGAAGCCGCTGCTGCT 1462
QY 1141 GGGAGATCTCTGATACACCTTGACATCCAGCCACAGGCAAGGTCATGGCTGAGGTGAAC 1200
Db 1463 GGGAGATCTCTGATACACCTTGACATCCAGCCACAGGCAAGGTCATGGCTGAGGTGAAC 1522
QY 1201 AAGACCTTCAGGAACTGGCTGTGTTCATGATCTGGAAGCATGTGGAGGAACTCAGC 1260
Db 1523 AAGACCTTCAGGAACTGGCTGTGTTCATGATCTGGAAGCATGTGGAGGAACTCAGC 1582
QY 1261 CCCAAGATCTGACCTTCATGGAGAACAGCAAGAAATGACCTTTGCCGATGCTGTTG 1320
Db 1583 CCCAAGATCTGACCTTCATGGAGAACAGCAAGAAATGACCTTTGCCGATGCTGTTG 1642
QY 1321 GACAGCAGGGAACAATGACCACTTTTGGGAACAGCAGTTGATGGCTTTAGATTTGACAGCC 1380
Db 1643 GACAGCAGGGAACAATGACCACTTTTGGGAACAGCAGTTGATGGCTTTAGATTTGACAGCC 1702

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QY	1381	CAAGACATCGTGGCGTTTTTTGGCCAAAGCACCCAGAGGATCTCCAGTCCAGTAATGTTCTT	1440
Db	1703	CAAGACATCGTGGCGTTTTTTGGCCAAAGCACCCAGAGGATCTCCAGTCCAGTAATGTTCTT	1762
QY	1441	GTGTACACCTGGAGAGAGCTTTCAACCAGAGACTAACACGGCAATCCGGAGCCATATCTCG	1500
Db	1763	GTGTACACCTGGAGAGAGCTTTCAACGAGACTAACACGGCAATCCGGAGCCATATCTCG	1822
QY	1501	TTCATGGAGTGTCTCAACCTGAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC	1560
Db	1823	TTCATGGAGTGTCTCAACCTGAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC	1882
QY	1561	AACAAGTCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTTGTTCACTGGA	1620
Db	1883	AACAAGTCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTTGTTCACTGGA	1942
QY	1621	ATTACTCCAGGAGCATTCAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1680
Db	1943	ATTACTCCAGGAGCATTCAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	2002
QY	1681	GACAATGTGGAGAGCAAAATAAATCAAGATGGGTACTGGGACCTGGTCTCTCAGCT	1740
Db	2003	GACAATGTGGAGAGCAAAATAAATCAAGATGGGTACTGGGACCTGGTCTCTCAGCT	2062
QY	1741	GACCCCTTTGAGGACATGGGTACGTTCTGGGGGCTTCGCTACTTTGCAGGATGTGCTG	1800
Db	2063	GACCCCTTTGAGGACATGGGTACGTTCTGGGGGCTTCGCTACTTTGCAGGATGTGCTG	2122
QY	1801	GAGCAGCCAATCATCAGGTGCTGACGGGCAACCGAGAAAGAAACTGGTCTATATGCAA	1860
Db	2123	GAGCAGCCAATCATCAGGTGCTGACGGGCAACCGAGAAAGAAACTGGTCTATATGCAA	2182
QY	1861	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCGGGTGATGACCCGGTCAATG	1920
Db	2183	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCGGGTGATGACCCGGTCAATG	2242
QY	1921	CCCTCTTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1980
Db	2243	CCCTCTTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	2302
QY	1981	TATGAGAGAGGACCGCTGAAAGAGACCATGCGGATCATGGCCTGGACACAGCATATA	2040
Db	2303	TATGAGAGAGGACCGCTGAAAGAGACCATGCGGATCATGGCCTGGACACAGCATATA	2362
QY	2041	CTCTGGTTTACGTGGTTTCATTAGTAGCCCTCATCTCCTCTTGTGTGAGCGCTGGCCTGCTA	2100
Db	2363	CTCTGGTTTACGTGGTTTCATTAGTAGCCCTCATCTCCTCTTGTGTGAGCGCTGGCCTGCTA	2422
QY	2101	GTGTGTACCTGAAGTTAGAAACCTGTGCGCCTACAGTATCCAGCGGTGGTGTGTC	2160
Db	2423	GTGTGTACCTGAAGTTAGAAACCTGTGCGCCTACAGTATCCAGCGGTGGTGTGTC	2482
QY	2161	TTCTGTGCGGTGTTGCTGTGGTGCAACTCCTGCACTGCTTCCCTGATTAGCACACTCTTC	2220
Db	2483	TTCTGTGCGGTGTTGCTGTGGTGCAACTCCTGCACTGCTTCCCTGATTAGCACACTCTTC	2542
QY	2221	TCCAGAGCCCAACTGGCAGACGCTGTGGGGCATCATCTACTTACGCTGTACCTGCC	2280
Db	2543	TCCAGAGCCCAACTGGCAGACGCTGTGGGGCATCATCTACTTACGCTGTACCTGCC	2602
QY	2281	TACGTCTCTGTGTGGCATGGCAGGACTACGTGGCCTTCACACTCAAGATCTTCGCTAGC	2340
Db	2603	TACGTCTCTGTGTGGCATGGCAGGACTACGTGGCCTTCACACTCAAGATCTTCGCTAGC	2662
QY	2341	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGACAG	2400
Db	2663	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGACAG	2722
QY	2401	GGCATTTGGATGGAGTGGGACAAACCTGTTTGAGATGCTCTGTGGAGGAAGATGGCTCAAT	2460
Db	2723	GGCATTTGGATGGAGTGGGACAAACCTGTTTGAGATGCTCTGTGGAGGAAGATGGCTCAAT	2782

Qy	2461	CTCACCACCTTCGATCCCAATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2520
Db	2783	CTCACCACCTTCGATCCCAATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2842
Qy	2521	TACATTGAGGCTGCTTTCCAGCGCAGTACGGAATCCAGGCGCCTGGTATTTTCCTTGC	2580
Db	2843	TACATTGAGGCTGCTTTCCAGCGCAGTACGGAATCCAGGCGCCTGGTATTTTCCTTGC	2902
Qy	2581	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGACCCACCTGGTCCAAACCAG	2640
Db	2903	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGACCCACCTGGTCCAAACCAG	2962
Qy	2641	AAGAGATGTCAGAAATCTGCATGGAGGAGGAACCCACCTTGAAGCTGGGCGTGCTC	2700
Db	2963	AAGAGATGTCAGAAATCTGCATGGAGGAGGAACCCACCTTGAAGCTGGGCGTGCTC	3022
Qy	2701	ATTCCAGAACCTGTTAAAGTCTACCGAGATGGATGAAGTGGGTGCTGATGGCCTGGCA	2760
Db	3023	ATTCCAGAACCTGTTAAAGTCTACCGAGATGGATGAAGTGGGTGCTGATGGCCTGGCA	3082
Qy	2761	CTGAATTTTTATGAGGCCAGATCACCTCCCTTCCTGGCCACATGAGCGGGGAAGCG	2820
Db	3083	CTGAATTTTTATGAGGCCAGATCACCTCCCTTCCTGGCCACATGAGCGGGGAAGCG	3142
Qy	2821	ACCACCATGTCATCTGACCGGGTGTTCCTCCCGACCTCGGCCACCGCTACATCCTG	2880
Db	3143	ACCACCATGTCATCTGACCGGGTGTTCCTCCCGACCTCGGCCACCGCTACATCCTG	3202
Qy	2881	GGAAAGACATTCGTCTTGATGAGCACCATCCCGGAGAACCTGGGGGTCTGTCCCCAG	2940
Db	3203	GGAAAGACATTCGTCTTGATGAGCACCATCCCGGAGAACCTGGGGGTCTGTCCCCAG	3262
Qy	2941	CATAACGTGCTGTTGACATGCTGACTGTCGAAGAACACATCTGGTTCATGCCCCGTG	3000
Db	3263	CATAACGTGCTGTTGACATGCTGACTGTCGAAGAACACATCTGGTTCATGCCCCGTG	3322
Qy	3001	AAAGGGCTCTCTGAGAAGCAGCTGAAGCGGGAGATGGAGCAGATGGCCCTGGATGTGGT	3060
Db	3323	AAAGGGCTCTCTGAGAAGCAGCTGAAGCGGGAGATGGAGCAGATGGCCCTGGATGTGGT	3382
Qy	3061	TTGCCATCAAGCAGCTGAAACCAAAACCAAGCAGCTGTCAAGTGGAAATCCACGAGAAG	3120
Db	3383	TTGCCATCAAGCAGCTGAAACCAAAACCAAGCAGCTGTCAAGTGGAAATCCACGAGAAG	3442
Qy	3121	CTATCTGTGGCCTTGGCCTTTGTGGGGGATCTAAGGTTGTCAATCTGGATGAACCCACA	3180
Db	3443	CTATCTGTGGCCTTGGCCTTTGTGGGGGATCTAAGGTTGTCAATCTGGATGAACCCACA	3502
Qy	3181	GCTGGTGTGACCTTACTCCCGCAGGGAATATGGAGCTGCTGCTGAATACCCGACAA	3240
Db	3503	GCTGGTGTGACCTTACTCCCGCAGGGAATATGGAGCTGCTGCTGAATACCCGACAA	3562
Qy	3241	GGCGCAGCAATATTCTCTACACACCACATGGATGAAGCGAGCTCCTGGGGACAGG	3300
Db	3563	GGCGCAGCAATATTCTCTACACACCACATGGATGAAGCGAGCTCCTGGGGACAGG	3622
Qy	3301	ATTGGCATCATCTCCCATGGGAGCTGTGGTGTGGGGCTCCTCCTGTTTCTCAAGAAC	3360
Db	3623	ATTGGCATCATCTCCCATGGGAGCTGTGGTGTGGGGCTCCTCCTGTTTCTCAAGAAC	3682
Qy	3361	CAGCTGGGAACAGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCTCAGT	3420
Db	3683	CAGCTGGGAACAGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCTCAGT	3742
Qy	3421	TCTTCGAAACAGTAGTAGCACTGTGTCTATCCTGAAAAAGGAGACAGTGTTCCTCAG	3480
Db	3743	TCTTCGAAACAGTAGTAGCACTGTGTCTATCCTGAAAAAGGAGACAGTGTTCCTCAG	3802
Qy	3481	AGCAGTCTGATGCTGCCTGGCGACCATGAGAGTGACACCTGACCATCGATGTC	3540
Db	3803	AGCAGTCTGATGCTGCCTGGCGACCATGAGAGTGACACCTGACCATCGATGTC	3862
Qy	3541	TCTGTATCTCCCAACCTCATCAGGAAGCATGTCTGTAAGCCCGCTGGTGGAAACATA	3600

Db 3863 TCTGCTAATCTCAACCTCATCAGGAACATGTCTGAAGCCGGCTGTGGAGACATA 3922
QY 3601 GGGCATGAGCTGACCTATGTCTGCCATATGAAGCTCTTAAGAGAGGAGCCTTTGTGGAA 3660
Db 3923 GGGCATGAGCTGACCTATGTCTGCCATATGAAGCTCTTAAGAGAGGAGCCTTTGTGGAA 3982
QY 3661 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3720
Db 3983 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 4042
QY 3721 GAGACGACCTGGGAAGAAATATCTCAAGTGGCCGAGAGAGTGGGTGATGCTGAG 3780
Db 4043 GAGACGACCTGGGAAGAAATATCTCAAGTGGCCGAGAGAGTGGGTGATGCTGAG 4102
QY 3781 ACCTCAGATGGTACCTTGGCAGCAAGACGAGCGGGCCCTTCGGGACAAAGCAGAGC 3840
Db 4103 ACCTCAGATGGTACCTTGGCAGCAAGACGAGCGGGCCCTTCGGGACAAAGCAGAGC 4162
QY 3841 TGTCTTCGCCCGTTCAGTGAAGATGATGCTGCTGATGCCAATGATTTCTGACATAGACCA 3900
Db 4163 TGTCTTCGCCCGTTCAGTGAAGATGATGCTGCTGATGCCAATGATTTCTGACATAGACCA 4222
QY 3901 GAATCCAGAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAGGGTCTTACCAGGTGAAA 3960
Db 4223 GAATCCAGAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAGGGTCTTACCAGGTGAAA 4282
QY 3961 GGCTGGAACTTACACAGAACAGTTTGTGGCCCTTTGTGGAGAGACTGCTAATGGC 4020
Db 4283 GGCTGGAACTTACACAGAACAGTTTGTGGCCCTTTGTGGAGAGACTGCTAATGGC 4342
QY 4021 AGACGGAGTCGGAAGAGATTTTGTCTCAGATGCTCTGCCAGCTGTGTTGTCTCATTT 4080
Db 4343 AGACGGAGTCGGAAGAGATTTTGTCTCAGATGCTCTGCCAGCTGTGTTGTCTCATTT 4402
QY 4081 GCCTTGTGTTACGCTGATGCTGTCACACCTTTGGCAAGTACCCAGCCTGGAACCTTCA 4140
Db 4403 GCCTTGTGTTACGCTGATGCTGTCACACCTTTGGCAAGTACCCAGCCTGGAACCTTCA 4462
QY 4141 CCCTGGATGTACAAACAGTACACATTTGTGCAAGATGATGCTCTCAGGACAGGGA 4200
Db 4463 CCCTGGATGTACAAACAGTACACATTTGTGCAAGATGATGCTCTCAGGACAGGGA 4522
QY 4201 ACCCTGGAACCTTAAACGCCCTTACCAAGACCCCTGGCTTCCGGACCCGCTGTATGAA 4260
Db 4523 ACCCTGGAACCTTAAACGCCCTTACCAAGACCCCTGGCTTCCGGACCCGCTGTATGAA 4582
QY 4261 GGAACCCCAATCCAGACAGCCCTGCCAGCAGGGAGAGAGTGGACACTGCCCA 4320
Db 4583 GGAACCCCAATCCAGACAGCCCTGCCAGCAGGGAGAGAGTGGACACTGCCCA 4642
QY 4321 GTTCCCCAGACCATATGAGACCTTCTCCAGATGGGAATGGGAATGGGAATGGGAATGGGA 4380
Db 4643 GTTCCCCAGACCATATGAGACCTTCTCCAGATGGGAATGGGAATGGGAATGGGAATGGGA 4702
QY 4381 CTTGATCCAGTGTAGCAGCAAAATCAAGAAGATGCTGCCCTGTGTGTCCTCCAGG 4440
Db 4703 CTTGATCCAGTGTAGCAGCAAAATCAAGAAGATGCTGCCCTGTGTGTCCTCCAGG 4762
QY 4441 GCAGGGGGCTGCCCTCTCCACAAAGAAACAAAACACTGCAATATCTTCCAGGACCTG 4500
Db 4763 GCAGGGGGCTGCCCTCTCCACAAAGAAACAAAACACTGCAATATCTTCCAGGACCTG 4822
QY 4501 ACAGNAGAAACATTTCCGATTTATCTGTTGAGAGAGTATGTCAGATCATAGCCAAAAGC 4560
Db 4823 ACAGNAGAAACATTTCCGATTTATCTGTTGAGAGAGTATGTCAGATCATAGCCAAAAGC 4882
QY 4561 TTAAGAAACAAAGATCTGGGTGAATGAGTTAGTTAGTGGCGCTTTTCCCTGGGTGCTAGT 4620
Db 4883 TTAAGAAACAAAGATCTGGGTGAATGAGTTAGTTAGTGGCGCTTTTCCCTGGGTGCTAGT 4942
QY 4621 AATACATCAGCACTTCTCCGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAA 4680

Db 4943 AATACTCAAGCACTTCTCCGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAA 5002
QY 4681 CACCTTAAGCTGGCCAGGACAGATTTCTGAGATCGATTTCTCAACAGCTTGGAGAGATTT 4740
Db 5003 CACCTTAAGCTGGCCAGGACAGATTTCTGAGATCGATTTCTCAACAGCTTGGAGAGATTT 5062
QY 4741 ATGACAGGACTGGACACCAAAATATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT 4800
Db 5063 ATGACAGGACTGGACACCAAAATATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT 5122
QY 4801 GCAATCAGCTCTTCTGATGATGATCAACAATGCCATTTCCGGGGCCAACTGGCAAAAG 4860
Db 5123 GCAATCAGCTCTTCTGATGATGATCAACAATGCCATTTCCGGGGCCAACTGGCAAAAG 5182
QY 4861 GGAGAGAACCCCTAGCATTATGGAATTACTGCTTTCATCATCCCTCAATCTCACCAG 4920
Db 5183 GGAGAGAACCCCTAGCATTATGGAATTACTGCTTTCATCATCCCTCAATCTCACCAG 5242
QY 4921 CAGCAGCTCTCAGAGGTGGCTGTGATGACCAATCAGTGGATGCTTGTGCTGATGCTG 4980
Db 5243 CAGCAGCTCTCAGAGGTGGCTGTGATGACCAATCAGTGGATGCTTGTGCTGATGCTG 5302
QY 4981 GTCATCTTGTGCAATCTGCTTCCAGCAGCCTTGTGCTGATGCTTGTGCTGATGCTG 5040
Db 5303 GTCATCTTGTGCAATCTGCTTCCAGCAGCCTTGTGCTGATGCTTGTGCTGATGCTG 5362
QY 5041 GTCAGCAAGCAAAACACTGCAAGTTTCATGAGTGGAGTGAAGCCTGTCTACTTGGCTC 5100
Db 5363 GTCAGCAAGCAAAACACTGCAAGTTTCATGAGTGGAGTGAAGCCTGTCTACTTGGCTC 5422
QY 5101 TCTAATTTGTCTGGATATGTCGATGACATTTACGTTGCTGCTGCCACACTGGTCAATATC 5160
Db 5423 TCTAATTTGTCTGGATATGTCGATGACATTTACGTTGCTGCTGCCACACTGGTCAATATC 5482
QY 5161 TCTAATTTGTCTGGATATGTCGATGACATTTACGTTGCTGCTGCCACACTGGTCAATATC 5220
Db 5483 TCTAATTTGTCTGGATATGTCGATGACATTTACGTTGCTGCTGCCACACTGGTCAATATC 5542
QY 5221 CTACTTTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5280
Db 5543 CTACTTTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5602
QY 5281 AAGATCCCCAGCAGCAGCTATGCTGCTCACCAGGTGAAGCCTTCTCATTTGGCATTAAT 5340
Db 5603 AAGATCCCCAGCAGCAGCTATGCTGCTCACCAGGTGAAGCCTTCTCATTTGGCATTAAT 5662
QY 5341 GGCAGCTGGCCACTTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 5400
Db 5663 GGCAGCTGGCCACTTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAG 5722
QY 5401 GATATCTGGAAGTCCGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5460
Db 5723 GATATCTGGAAGTCCGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5782
QY 5461 GACATGTTGAAAAACAGGCAATGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5520
Db 5783 GACATGTTGAAAAACAGGCAATGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5842
QY 5521 GTGTCAACATATCTTGGACTTGGTGGAGCAACCTCTTCCCATGGCCGTGGAGAGG 5580
Db 5843 GTGTCAACATATCTTGGACTTGGTGGAGCAACCTCTTCCCATGGCCGTGGAGAGG 5902
QY 5581 GTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 5640
Db 5903 GTGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 5962
QY 5641 GTAATGCAAGCTATCT 5700
Db 5963 GTAATGCAAGCTATCT 6022
QY 5701 AGAATTTCTGATGCTGGAGGCCAGATGACATTTAGAAATCAAGGAGTTGACCAAGATA 5760
Db 6023 AGAATTTCTGATGCTGGAGGCCAGATGACATTTAGAAATCAAGGAGTTGACCAAGATA 6082

Qy	5761	TATAGAAGGAACGGGAAGCGTCTGTTGACAGAGATTTCGCTGGGCATTCCTCTCTGGTGAG	5820
Db	6083	TATAGAAGGAACGGGAAGCGTCTGTTGACAGAGATTTCGCTGGGCATTCCTCTCTGGTGAG	6142
Qy	5821	TGCTTTGGCTCCTGGGAGTTAATGGGCTGGAAATATCATCACTTTCAGATGTTAAACA	5880
Db	6143	TGCTTTGGCTCCTGGGAGTTAATGGGCTGGAAATATCATCACTTTCAGATGTTAAACA	6202
Qy	5981	GGAGATACCACGTGTTACCAGAGGAGATCTTTCCTTAAACAAAATAGTATCTTATCAAAAC	5940
Db	6203	GGAGATACCACGTGTTACCAGAGGAGATCTTTCCTTAAACAAAATAGTATCTTATCAAAAC	6262
Qy	5941	ATCCATGAAGTACATCAGNACATGGCTACGTGCCTCAGTTTGATGCCATCAGAGCTG	6000
Db	6263	ATCCATGAAGTACATCAGNACATGGCTACGTGCCTCAGTTTGATGCCATCAGAGCTG	6322
Qy	6001	TTGACTGGGAGAGAACACGTGAGTCTCTTTGCCCTTTTGAGAGAGTCCCGAGAGAAAGAA	6060
Db	6323	TTGACTGGGAGAGAACACGTGAGTCTCTTTGCCCTTTTGAGAGAGTCCCGAGAGAAAGAA	6382
Qy	6061	GTTGCGAAGTTGGTGAGTGGCGGATTTCGGAAACTGGGCCCTCGTAGTATGGAGAAAAA	6120
Db	6383	GTTGCGAAGTTGGTGAGTGGCGGATTTCGGAAACTGGGCCCTCGTAGTATGGAGAAAAA	6442
Qy	6121	TATGCTGGTAAGTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6443	TATGCTGGTAAGTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6502
Qy	6181	GGCGGGCCCTCTGTGTGTTTCTGATGAACCCACACAGGCATGGATCCCAAGCCCGG	6240
Db	6503	GGCGGGCCCTCTGTGTGTTTCTGATGAACCCACACAGGCATGGATCCCAAGCCCGG	6562
Qy	6241	CGGTTCTTGGAATTGCCCCTAAGTGTTGTCAGGAGGGAGATCAGTAGTCTTTACA	6300
Db	6563	CGGTTCTTGGAATTGCCCCTAAGTGTTGTCAGGAGGGAGATCAGTAGTCTTTACA	6622
Qy	6301	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGTCATATGGA	6360
Db	6623	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGTCATATGGA	6682
Qy	6361	AGGTTACAGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGGTTATACA	6420
Db	6683	AGGTTACAGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGGTTATACA	6742
Qy	6421	ATAGTTGTACGAATACAGGGTCCAAACCGGACCTTGAAGCCTGTCACAGATTTCTTTGGA	6480
Db	6743	ATAGTTGTACGAATACAGGGTCCAAACCGGACCTTGAAGCCTGTCACAGATTTCTTTGGA	6802
Qy	6481	CTTGCAATTTCCGGAAGTGTTCATAAGAGAAACACCGGACATGCTACAAATACAGCTT	6540
Db	6803	CTTGCAATTTCCGGAAGTGTTCATAAGAGAAACACCGGACATGCTACAAATACAGCTT	6862
Qy	6541	CCATCTTCATATCTTCTCTGGCCAGGATTTACAGCTCCTCTCCAGAGCAAAAACGGA	6600
Db	6863	CCATCTTCATATCTTCTCTGGCCAGGATTTACAGCTCCTCTCCAGAGCAAAAACGGA	6922
Qy	6601	CTCCACATAGAAGACTACTCTGTTTCTCAGCAACACTGTGACCAAGTATTTGTGAACCTT	6660
Db	6923	CTCCACATAGAAGACTACTCTGTTTCTCAGCAACACTGTGACCAAGTATTTGTGAACCTT	6982
Qy	6661	GCCANGACCAAGTGATGATGACCACTTAAAGAGCCCTCTCATTTACAAAAACCCAGACA	6720
Db	6983	GCCANGACCAAGTGATGATGACCACTTAAAGAGCCCTCTCATTTACAAAAACCCAGACA	7042
Qy	6721	GTAGTGGACCTTGCAGCTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	6780
Db	7043	GTAGTGGACCTTGCAGCTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	7102
Qy	6781	GTAT 6784	
Db	7103	GTAT 7106	

RESULT 8	AX092594	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
LOCUS	AX092594	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
DEFINITION	AX092594	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
ACCESSION	AX092594	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
VERSION	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
KEYWORDS	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
SOURCE	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
ORGANISM	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
REFERENCE	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
AUTHORS	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
TITLE	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
JOURNAL	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
FEATURES	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
BASE COUNT	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
ORIGIN	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
Query Match	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
Best Local Similarity	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
Mismatches	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
Conservative	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
Indels	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
Gaps	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
0;	AX092594.1	Sequence	7860 bp	DNA	linear	PAT 21-MAR-2001
1	ATGGCTGTGGCCCTCAGCTGAGTTGCTGCTGGAGAACCTCAGCTTCAGAGAAGA	60				
Db	75	ATGGCTGTGGCCCTCAGCTGAGTTGCTGCTGGAGAACCTCAGCTTCAGAGAAGA	134			
Qy	61	CAAAATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCTGATCTCTGATC	120			
Db	135	CAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTATTATCTTCTGATCTCTGATC	194			
Qy	121	TCTGTGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCC	180			
Db	195	TCTGTGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTTCCAAATAAAGCC	254			
Qy	181	ATGCCCTCTGCAGGACACTTCTTGGGTCAGGGGATATCTGTAATGCCAACACCC	240			
Db	255	ATGCCCTCTGCAGGACACTTCTTGGGTCAGGGGATATCTGTAATGCCAACACCC	314			
Qy	241	TGTTTCCGTTACCGACTCCTGGGAGGCTCCCGAGTTGTTGGAACTTTAACAAATCC	300			
Db	315	TGTTTCCGTTACCGACTCCTGGGAGGCTCCCGAGTTGTTGGAACTTTAACAAATCC	374			
Qy	301	ATTTGGCTGGCTGTTCTCAGATGCTCGAGAGCTCTTTTATACAGCCAGAAAGACCC	360			
Db	375	ATTTGGCTGGCTGTTCTCAGATGCTCGAGAGCTCTTTTATACAGCCAGAAAGACCC	434			
Qy	361	AGCATGAAGGATCGGCAAGTCTTGAGAACTTACAGCAGATCAAGAAATCCAGCTCA	420			
Db	435	AGCATGAAGGATCGGCAAGTCTTGAGAACTTACAGCAGATCAAGAAATCCAGCTCA	494			
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 9741)
AUTHORS Deneffe, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
TITLE Nucleic acids of the human abcl1 gene and their therapeutic and
diagnostic application
JOURNAL Patent: WO 0130848-A 69 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES Location/Qualifiers
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ACCESSION AX139817
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KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 9741)
AUTHORS Denefle,P., Roslier-Montus,M.F., Arnould-Reguigne,I., Prades,C.,
Naudin,L., Iemoline,C., Duverger,N., Jaye,M., searfoos III,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
TITLE Nucleic acids of the human abcl gene and their therapeutic and
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JOURNAL Patent: EP 1056012-A 69 02-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
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RESULT 14
AX127831
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 9854)
AUTHORS
Denefle, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Searfoss, G.H.,
Remaley, A., Brewer, H.B. and Dean, M.
Nucleic acids of the human abcl gene and their therapeutic and
diagnostic application
Patent: WO 0130848-A 70 03-MAY-2001;
Aventis Pharma S.A. (FR)
FEATURES
Location/Qualifiers
1..9854
/organism="Homo sapiens"

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ORIGIN						
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QY	2101	GTGGTCATCCTGAAGATTAGGAACCTTGTCGCCCTACAGTGCATCCACGCTGSGTGTTC	2160
Db	2398	GTGGTCATCCTGAAGATTAGGAACCTGCTGCCCTACAGTGATCCACGCTGSGTGTTC	2457
QY	2161	TTCCCTGTCGGTGTTCCTGTGGTGACAACTCTGCAGTGCCTTCCTGATTAGCACACTCTC	2220
Db	2458	TTCCCTGTCGGTGTTCCTGTGGTGACAACTCTGCAGTGCCTTCCTGATTAGCACACTCTC	2517
QY	2221	TCAGAGCCAACTCGCAGCAGCCTGTGGGGGCATCATCTACTTTCAGCTGTACCTGCC	2280
Db	2518	TCAGAGCCAACTCGCAGCAGCCTGTGGGGGCATCATCTACTTTCAGCTGTACCTGCC	2577
QY	2281	TAGCTCCTGTGTGGCGATGGCAGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2340
Db	2578	TAGCTCCTGTGTGGCGATGGCAGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2637
QY	2341	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGGCTTTTGGTGGAGAGCAG	2400
Db	2638	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGGCTTTTGGGAGGACG	2697
QY	2401	GGCATTGGAGTGCAGTGGGACAACTGTTTGAGAGTCTCTGTGGAGGAAGATGCGTTCAT	2460
Db	2698	GGCATTGGAGTGCAGTGGGACAACTGTTTGAGAGTCTCTGTGGAGGAAGATGCGTTCAT	2757
QY	2461	CTCACCACATTCGATCTCCATGATGCTGTTTGACACCTCTCTCTATGGGTGATGACCTGG	2520
Db	2758	CTCACCACATTCGCTCCCATGATGCTGTTTGACACCTCTCTCTATGGGTGATGACCTGG	2817
QY	2521	TACATTGAGCTGTCTTTCCAGGCCAGTACGGAATTCACGGCCCTCGTATTTTCCTTGC	2580
Db	2818	TACATTGAGCTGTCTTTCCAGGCCAGTACGGAATTCACGGCCCTCGTATTTTCCTTGC	2877
QY	2581	ACCAAGTCTACTGTTTGGCGAGGAAGTGATGAGAGAGCCACCTGGTTCACACCG	2640
Db	2878	ACCAAGTCTACTGTTTGGCGAGGAAGTGATGAGAGAGCCACCTGGTTCACACCG	2937
QY	2841	AAGAGAAATGTCAAAATCTGCATGGAGGAGGAACCCACCTTTGAAGCTGGCGTGCTCC	2700
Db	2938	AAGAGAAATGCAGAAATCTGCATGGAGGAGGAACCCACCTTTGAAGCTGGCGTGCTCC	2997
QY	2701	ATTTCAGAACCTGTTAAAGTCTACCGAGATGGGATGAGGTGGCTGTGCATGCCCTGGCA	2760
Db	2998	ATTTCAGAACCTGTTAAAGTCTACCGAGATGGGATGAGGTGGCTGTGCATGGCCTGGCA	3057
QY	2761	CTGAATTTTATGAGGCCAGATCACCTCTCTCTGGGCCACAATGGAGCGGGGAAGACG	2820
Db	3058	CTGAATTTTATGAGGCCAGATCACCTCTCTCTGGGCCACAATGGAGCGGGGAAGACG	3117
QY	2821	ACCACCATGTCAATCTGCACCGGTTGTTCCCGCAGCCTCGGGCAGCGCCTACATCCTG	2880
Db	3118	ACCACCATGTCAATCTGCACCGGTTGTTCCCGCAGCCTCGGGCAGCGCCTACATCCTG	3177
QY	2881	GGAAAAGACATTCGCTCTCAGATGAGCACCATCCGGCAGAACCTTGGGGTCTGTCCCCAG	2940
Db	3178	GGAAAAGACATTCGCTCTCAGATGAGCACCATCCGGCAGAACCTTGGGGTCTGTCCCCAG	3237
QY	2941	CATAACGTGCTGTTTGACATGCTGACTGTGCGAAGAACACATCTGGTTCATGCCCGTTG	3000
Db	3238	CATAACGTGCTGTTTGACATGCTGACTGTGCGAAGAACACATCTGGTTCATGCCCGTTG	3297
QY	3001	AAAGGGCTCTCTCAGAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3060
Db	3298	AAAGGGCTCTCTCAGAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3357
QY	3061	TTGGCATCAAGCAAGCTGAAAAGCAAAACAGCCAGCTGTCTCAGTGGGAATCCAGAGAAAG	3120
Db	3358	TTGGCATCAAGCAAGCTGAAAAGCAAAACAGCCAGCTGTCTCAGTGGGAATCCAGAGAAAG	3417
QY	3121	CTATCTGTGGCCTTGGCCTTTGTGGGGGATCTAAGGTTGTCAATCTCGATGAACCCACA	3180
Db	3418	CTATCTGTGGCCTTGGCCTTTGTGGGGGATCTAAGGTTGTCAATCTCGATGAACCCACA	3477

Qy	3181	GCTGGTGTGACCCCTTACTCCCGCAGGGGAAATATGGGAGCTGCTGCTGAATACCACAA	3240
Db	3478	GCTGGTGTGACCCCTTACTCCCGCAGGGGAAATATGGGAGCTGCTGCTGAATACCACAA	3537
Qy	3241	GGCGCACCATTATCTCTCTACACACCATGGATGAAGCGGACGTCCTGGGGGACAGG	3300
Db	3538	GGCGCACCATTATCTCTCTACACACCATGGATGAAGCGGACGTCCTGGGGGACAGG	3597
Qy	3301	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGGGCTCCTCCCTGTTCTTGAAAGAC	3360
Db	3598	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGGGCTCCTCCCTGTTCTTGAAAGAC	3657
Qy	3361	CAGCTGGGAACAGGCTACTACCTTGCTTCAAGAAGAATGTGGAATCCTCCCTCAGT	3420
Db	3658	CAGCTGGGAACAGGCTACTACCTTGCTTCAAGAAGAATGTGGAATCCTCCCTCAGT	3717
Qy	3421	TCCTGCAGAAACAGTAGTAGCAGCTGTGTACACTGAAAAAGGAGGACAGTGTTCAC	3480
Db	3718	TCCTGCAGAAACAGTAGTAGCAGCTGTGTACACTGAAAAAGGAGGACAGTGTTCAC	3777
Qy	3481	AGCAGTTCTGATGCTGGCTGGGACGACCATGAGAGTGACACGCTGACCATCGATGTC	3540
Db	3778	AGCAGTTCTGATGCTGGCTGGGACGACCATGAGAGTGACACGCTGACCATCGATGTC	3837
Qy	3541	TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGGTGGAGACATA	3600
Db	3838	TCTGCTATCTCCAACTCATCAGGAAGCATGTGCTGAAGCCCGCTGGTGGAGACATA	3897
Qy	3601	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGAGGACCTTTGTGAA	3660
Db	3898	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGAGGACCTTTGTGAA	3957
Qy	3661	CTCTTTTCATGAGATTGATGACGGCTCTCAGACCTTGGCATTCTTAGTTATGGCATCTCA	3720
Db	3958	CTCTTTTCATGAGATTGATGACGGCTCTCAGACCTTGGCATTCTTAGTTATGGCATCTCA	4017
Qy	3721	GAGACGACCCCTGGAAGAAATATTCCCTCAAGTGGCCGAAGAGAGTGGGTGGATGCTGAG	3780
Db	4018	GAGACGACCCCTGGAAGAAATATTCCCTCAAGTGGCCGAAGAGAGTGGGTGGATGCTGAG	4077
Qy	3781	ACCTCAGATGGTACCTTGCCAGCAACAGCAACAGCCGGGCTTCGGGACCAACGACAGC	3840
Db	4078	ACCTCAGATGGTACCTTGCCAGCAACAGCAACAGCCGGGCTTCGGGACCAACGACAGC	4137
Qy	3841	TGCTCTGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATCTTGACATAGACCCA	3900
Db	4138	TGCTCTGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATCTTGACATAGACCCA	4197
Qy	3901	GAATCCAGAGACAGACTTGCTCACTGGGATGGATGCGCAAGGCTCCTACCAGTGCAA	3960
Db	4198	GAATCCAGAGACAGACTTGCTCACTGGGATGGATGCGCAAGGCTCCTACCAGTGCAA	4257
Qy	3961	GGCTGGAACTTACACAGCAACAGTTGTGGCCCTTTTGTGGAAGAGACTGCTAAATGCC	4020
Db	4258	GGCTGGAACTTACACAGCAACAGTTGTGGCCCTTTTGTGGAAGAGACTGCTAAATGCC	4317
Qy	4021	AGACGGAGTGGGAAGGATTTTGTGCTCAGATTGCTTCCAGCTGTCTTTGTCTGCATT	4080
Db	4318	AGACGGAGTGGGAAGGATTTTGTGCTCAGATTGCTTCCAGCTGTCTTTGTCTGCATT	4377
Qy	4081	GGCCTTGTGTTCAACCCTGATCGTGCCACCTTTGGCAAGTACCCACGCTGGAATCTCAG	4140
Db	4378	GGCCTTGTGTTCAACCCTGATCGTGCCACCTTTGGCAAGTACCCACGCTGGAATCTCAG	4437
Qy	4141	CCCTGGATGTACAAGCAACAGTACATTTGTTCAGCAATGATGCTCTGAGGACACGGGA	4200
Db	4438	CCCTGGATGTACAAGCAACAGTACATTTGTTCAGCAATGATGCTCTGAGGACACGGGA	4497
Qy	4201	ACCCTGGAACTCTTAAACGGCCCTCACCAAGACCCCTGGCTTCGGGACCCGCTGTATGAA	4260
Db	4498	ACCCTGGAACTCTTAAACGGCCCTCACCAAGACCCCTGGCTTCGGGACCCGCTGTATGAA	4557

Db	6718	ATAGTTGTACGAATAGCAGGGTCCAAACCGGAACTGAGCGCTGTCCAGGATTTCTTTGGA	6777
Qy	6481	CTTCATTTCTGGAAGTGTCTAAAAGAGAAACACCGGAAACATGCTACAAATACCACTT	6540
Db	6778	CTTCATTTCTGGAAGTGTCTCAARAGAGAAACACCGGAAACATGCTACAAATACCACTT	6837
Qy	6541	CCATCTTCATATCTTCTCTGGCCAGGATATTCAGCATCTCTCTCCAGAGCAAAAACGGA	6600
Db	6838	CCATCTTCATATCTTCTCTGGCCAGGATATTCAGCATCTCTCTCCAGAGCAAAAACGGA	6897
Qy	6601	CTCCACATAGAAAGACTACTCTGTTTCTCAGACAAACACTTGACCAAGTATTTGTGAACCTT	6660
Db	6898	CTCCACATAGAAAGACTACTCTGTTTCTCAGACAAACACTTGACCAAGTATTTGTGAACCTT	6957
Qy	6661	GCCAAGGACCAAGTGATGATGACCATTTAAAGACCTCTCATTTACACAAAACCGACAGA	6720
Db	6958	GCCAAGGACCAAGTGATGATGACCATTTAAAGACCTCTCATTTACACAAAACCGACAGA	7017
Qy	6721	GTAGTGGACGTTGAGTTCACATCTTTCTACAGATGAGAAAGTGAAGAAAGCTAT	6780
Db	7018	GTAGTGGACGTTGAGTTCACATCTTTCTACAGATGAGAAAGTGAAGAAAGCTAT	7077
Qy	6781	GTAT 6784	
Db	7078	GTAT 7081	
RESULT 15			
AX139818			
LOCUS	AX139818	9854 bp	DNA linear PAT 30-MAY-2001
DEFINITION	Sequence 70 from Patent EP1096012.		
ACCESSION	AX139818		
VERSION	AX139818.1	GI:14275400	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 9854) Deneff, P., Rosier-Montus, M.F., Arnould-Reguigne, I., Prades, C., Naudin, L., Lemoine, C., Duverger, N., Jaye, M., searfof Iii, G.H., Remaley, A., Brewer, H.B. and Dean, M.		
TITLE	Nucleic acids of the human abcl gene and their therapeutic and diagnostic application		
JOURNAL	Patent: EP 1096012-A 70 02-MAY-2001;		
FEATURES	Aventis Pharma S.A. (FR) location/Qualifiers 1..9854 /organism="Homo sapiens" /db_xref="taxon:9606"		
BASE COUNT	2665 a 2219 c 2334 g 2635 t	1 others	
ORIGIN			
Query Match	99.7%;	Score 6764.8;	DB 6; Length 9854;
Best Local Similarity	99.8%;	Pred. No. 0;	
Matches 6772;	Conservative	0; Mismatches 12;	Indels 0; Gaps 0;
Qy	1	ATGGCTTTGTGGCCCTCAGCTGAGGTGCTGTGCGAAGAACCTCACATTTTCAGAGAAGA	60
Db	298	ATGGCTTTGTGGCCCTCAGCTGAGGTGCTGTGCGAAGAACCTCACATTTTCAGAGAAGA	357
Qy	61	CAACATGTCAGCTGTTACTGGAAGTGGCCCTGCTATTTATCTTCTGTATCTGATC	120
Db	358	CAACATGTCAGCTGCTGCTGGAAGTGGCCCTGCTATTTATCTTCTGTATCTGATC	417
Qy	121	TCTGTTTCGGCTGAGCTACCCACCTTATGAACAAATGAATGCCATTTTCCAAATAAAGCC	180
Db	418	TCTGTTTCGGCTGAGCTACCCACCTTATGAACAAATGAATGCCATTTTCCAAATAAAGCC	477
Qy	181	ATGCCCTCTGCAGGAACACTTCTTTGGGTTTCAGGGATATCTGTAATGCCAACACCC	240
Db	478	ATGCCCTCTGCAGGAACACTTCTTTGGGTTTCAGGGATATCTGTAATGCCAACACCC	537

Db.	1616	GAACAGGGACATGACCACTTTTGGGAACAGACGTTCGGATGGCTTAGATTGGACAGCC	16177
QY	1381	CAAGACATCGTGGGGTTTTTGGCCCAAGCACCCAGAGAGATGCCACGTACCAGTAATGGTTCCT	1440
Db	1678	CAAGACATCGTGGCGTTTGGGCCAAGCACCCAGAGAGATGCCACGTACCAGTAATGGTTCCT	1737
QY	1441	GTGTACACCTGGAGAGAGACTTTTCAAGGAGACTAACAGGCAATCCGAGCAATATCTCGC	1500
Db	1738	GTGTACACCTGGAGAGAGACTTTCAAGGAGACTAACAGGCAATCCGAGCAATATCTCGC	1797
QY	1501	TTTACTGGAGTGTCTCAACCTGAAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC	1560
Db	1798	TTTACTGGAGTGTCTCAACCTGAAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC	1857
QY	1561	AACAAGTCCATGGAGCTGTGGATGAGAGGAAGTTCTGGCTGSPATTGTTCACCTGGA	1620
Db	1858	AACAAGTCCATGGAGCTGTGGATGAGAGGAAGTTCTGGCTGSPATTGTTCACCTGGA	1917
QY	1621	ATTACTCCAGCAGCATTTGAGCTGCCCATCATGATCAAGTACAGATCCGAAATGGACATT	1680
Db	1918	ATTACTCCAGCAGCATTTGAGCTGCCCATCATGATCAAGTACAGATCCGAAATGGACATT	1977
QY	1681	GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCTGGTCTCGAGCT	1740
Db	1978	GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCTGGTCTCGAGCT	2037
QY	1741	GACCCCTTTGAGGACATGCGGTACGTTCTGGGGGGCTTCGGCTACTTGCAGAGATGGGT	1800
Db	2038	GACCCCTTTGAGGACATGCGGTACGTTCTGGGGGGCTTCGGCTACTTGCAGAGATGGGT	2097
QY	1801	GAGCAGGCAATCATCAGGGTGTCTGACGGGCACCCAGAGAGAAAATGGTGTCTATATGCAA	1860
Db	2098	GAGCAGGCAATCATCAGGGTGTCTGACGGGCACCCAGAGAGAAAATGGTGTCTATATGCAA	2157
QY	1861	CAGATGCCCTATCCCTGTACGTTGATGACATCTTCTCGGGGTGATGACCGGTCAATG	1920
Db	2158	CAGATGCCCTATCCCTGTACGTTGATGACATCTTCTCGGGGTGATGACCGGTCAATG	2217
QY	1921	CCCCTCTTCATGACGCTGGCCCTGGAATTTACTCAGTGGCTGTGATCATCAAGGCATCGTG	1980
Db	2218	CCCCTCTTCATGACGCTGGCCCTGGAATTTACTCAGTGGCTGTGATCATCAAGGCATCGTG	2277
QY	1981	TATGAGAGAGGACGGCTGAAGAGACCATTCGGGATCATGGCCCTGGACAAACAGATA	2040
Db	2278	TATGAGAGAGGACGGCTGAAGAGACCATTCGGGATCATGGCCCTGGACAAACAGATA	2337
QY	2041	CTCTGGTTTAGCTGGTTTCATTAGTAGCTCATCTCCTCTCTGTGAGCGCTGCCCTGCTA	2100
Db	2338	CTCTGGTTTAGCTGGTTTCATTAGTAGCTCATCTCCTCTCTGTGAGCGCTGCCCTGCTA	2397
QY	2101	GTGTGTCATCTGAAGTTAGAAACCTGTCGCCACAGTCAATCCACGCTGGTGTTCGTC	2160
Db	2398	GTGTGTCATCTGAAGTTAGAAACCTGTCGCCACAGTCAATCCACGCTGGTGTTCGTC	2457
QY	2161	TTCTCTGCGGTGTTCTGCTGTGTGACAACTCTGCAAGTCTCTTGATTAGCACACTCTTC	2220
Db	2458	TTCTCTGCGGTGTTCTGCTGTGTGACAACTCTGCAAGTCTCTTGATTAGCACACTCTTC	2517
QY	2221	TCCAGAGCCAACTGGCAGCAGCCCTGGGGGCAATCATCTACTTCAGCTGTACCTGCC	2280
Db	2518	TCCAGAGCCAACTGGCAGCAGCCCTGGGGGCAATCATCTACTTCAGCTGTACCTGCC	2577
QY	2281	TAGCTCCTGTGTGTGGCATGGCAGACACTACGTGGGCTTCACTCAAGATCTTTCGTAGC	2340
Db	2578	TAGCTCCTGTGTGTGGCATGGCAGACACTACGTGGGCTTCACTCAAGATCTTTCGTAGC	2637
QY	2341	CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTCGCCCTTTTGGAGAGAG	2400
Db	2638	CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTCGCCCTTTTGGAGAGAG	2697
QY	2401	GGCATTTGGAGTGCAGTGGACAACTGTTTGGAGTCCCTGTGGAGGAAGATGGCTCAAT	2460

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3661 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3720
3958 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 4017
3721 GAGACGACCTCGAAGAAATATTCCTCAAGTGGCCGGAAGAGTGGGGTGGATCGTCA 3780
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3781 ACCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3840
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3841 TGTCTCGCCGCTTCACTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3900
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4021 AGACGAGTGGGAAAGATTTTGTCTCAGATGATGATGATGATGATGATGATGATGATGATGAT 4080
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4141 CCCTGGATGTACAACGAAACAGTACATTTGTGTCAGATGATGATGATGATGATGATGATGATGAT 4200
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4201 ACCTGGAACTTTAAACGCTCACCAGGAGCCCTGGGATGGGATGGGATGGGATGGGATGGGAT 4260
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4621 AATACTCAAGCACCTTCTCCGAGTCAAGAAAGTTAATGATGCCATCAAAACAAATCAAGAAA 4680
4918 AATACTCAAGCACCTTCTCCGAGTCAAGAAAGTTAATGATGCCATCAAAACAAATCAAGAAA 4977
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5701 AGAATTTCTGATGGTGGAGGCCAGAAATGACATTTAGAAATCAAGAGTGTGACGAGATA 5760

Db	5998	AGAAATCTTGGATGGTGGAGCCAGAAATGACATCTTAGAAATCAAGAGTTGACGAAGATA	6057
QY	5761	TATAGAAGGAAGCGAAGCCTGCTGTGACAGGATTTGGTGGGCATTCCTCTGCTGAG	5820
Db	6058	TATAGAAGGAAGCGAAGCCTGCTGTGACAGGATTTGGTGGGCATTCCTCTGCTGAG	6117
QY	5821	TGCTTTGGGCTCCTGGGAGTTAATGGGCTGGAAATCAATCAACTTCAAGATGTTACA	5880
Db	6118	TGCTTTGGGCTCCTGGGAGTTAATGGGCTGGAAATCAATCAACTTCAAGATGTTACA	6177
QY	5881	GGAGATACCACCTGTTACACAGAGAGATGCTTCCCTTAACAAAAATAGTATCTTACAAC	5940
Db	6178	GGAGATACCACCTGTTACACAGAGAGATGCTTCCCTTAACAAAAATAGTATCTTACAAC	6237
QY	5941	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCACAGAGCTG	6000
Db	6238	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCACAGAGCTG	6297
QY	6001	TTGACTGGGAGAGACACGCTGGAGTTCTTTGCCCTTTTGAGAGAGTCCCGAGAAAGNA	6060
Db	6298	TTGACTGGGAGAGACACGCTGGAGTTCTTTGCCCTTTTGAGAGAGTCCCGAGAAAGNA	6357
QY	6061	GTGGCAAGTTGGTGGAGTGGCGCATCGGAACTGGGCTCGTGAAGTATGGAGAAAAA	6120
Db	6358	GTGGCAAGTTGGTGGAGTGGCGCATCGGAACTGGGCTCGTGAAGTATGGAGAAAAA	6417
QY	6121	TATGCTGTAACTATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6418	TATGCTGTAACTATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGGCTTTGATC	6477
QY	6181	GGCGGCTCTCTGTGTGTCTGGATGAACCCACACAGCATGGATCCCAAGCCCGG	6240
Db	6478	GGCGGCTCTCTGTGTGTCTGGATGAACCCACACAGCATGGATCCCAAGCCCGG	6537
QY	6241	CGGTTCTGTGAAGTATGCTTAAAGTGGTTCAGAGGAGGAGATCAGTAGTGTACA	6300
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QY	6421	ATAGTTGTACGAATAGCAGGTCCTAAGCTCTTGCATAGGATGGCAATCATGTCATATGA	6480
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QY	6781	GTAT 6784	

Db 7078 GTAT 7081

Search completed: April 3, 2003, 22:04:40
Job time : 13523.6 Secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 1141.31 Seconds
(without alignments)
13386.024 Million cell updates/sec

Title: US-09-595-526c-1_copy_291_7074

Perfect score: 6784

Sequence: 1 atgscgtgtggcctcagct.....agtgaagaagactatgtat 6784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6784	100.0	10442	22	AAF24680
2	6784	100.0	10442	22	AAF24702
3	6782.4	100.0	10474	22	AAF24685
4	6782.4	100.0	10474	22	AAF24686
5	6782.4	100.0	10474	22	AAF24707
6	6782.4	100.0	10474	22	AAF24708
7	6776	99.9	7860	22	AAF92835
8	6772.8	99.8	7860	22	AAF83826
9	6768	99.8	7260	22	AAD21326

10	6768	99.8	7260	22	AAI70315	Human ATP binding
11	6764.8	99.7	9741	22	AA506120	Human ABC1 DNA seq
12	6764.8	99.7	9741	24	AAD37273	Human ABC1 full-le
13	6764.8	99.7	9854	22	AA506121	Human ABC1 DNA seq
14	6763.2	99.7	7281	22	AAK51683	Human polynucleoti
15	6762.2	99.7	7086	22	ABA09200	Human ABCA1 homolo
16	6762.2	99.7	7086	22	AAK52667	Human polynucleoti
17	6742	99.4	7864	21	AAC69120	Human ABC1 choles
18	6740.4	99.4	7864	21	AAC69385	Human ABC1 choles
19	6740.4	99.4	7864	21	AAC69386	Human ABC1 choles
20	6740.4	99.4	7864	21	AAC69389	Human ABC1 choles
21	6726	99.1	7861	21	AAC69387	Human ABC1 choles
22	6718	99.0	7857	21	AAC69388	Human ABC1 choles
23	6708	98.9	6880	21	AAZ94734	Human ATP binding
24	6708	98.9	6880	22	AAI70314	Human ATP binding
25	6704.8	98.8	6880	22	AAD21325	Human ATP binding
26	1926.8	28.4	7323	21	AAZ94746	Human ATP binding
27	1926.8	28.4	7784	19	AAV33392	ATP binding cass
28	1904.4	28.1	5097	22	AAI93913	Human stomach can
29	1904.4	28.1	5097	22	AAH18233	Human ABCA7 sequ
30	1742.2	25.7	7795	24	ABL57810	Human ABCA7 codi
31	1737.4	25.6	6791	24	AAI44693	Human transporter
32	1735.8	25.6	6522	22	AA508706	Human PD-ATP-bind
33	1735.8	25.6	6768	24	AAI92007	Human PD-ATP-bind
34	1696	25.0	6607	22	AAF54812	DNA encoding human
35	1531.6	22.6	5762	22	AAF54792	Nucleotide sequ
36	1528.8	22.5	5811	22	AAD05626	Human secreted pro
37	1465	21.6	5669	22	AA508707	Human PD-ATP-bind
38	985	14.5	7610	24	AAD36299	Human transporter
39	985	14.5	8040	22	AAF57452	Human ABCA2 transp
40	985	14.5	8195	22	AAH75187	Nucleotide sequ
41	985	14.5	8269	24	ABL33009	Human ATP binding
42	974.4	14.4	5540	24	AAD27271	Human transporter
43	953.6	14.1	6792	22	AAD02722	Human ATP binding
44	949.2	14.0	3437	23	AA573965	DNA encoding novel
45	949.2	14.0	4413	23	AA583715	DNA encoding novel

ALIGNMENTS

RESULT 1

AAF24680

ID AAF24680 standard; DNA; 10442 BP.

XX AAF24680;

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of a human ABC1 polypeptide.

XX Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS

XX 291..7076

XX /*tag= a

XX /product= "ABC1 polypeptide"

XX WO200078972-A2.

XX 28-DEC-2000.

XX 16-JUN-2000; 2000WO-US15765.

XX 18-JUN-1999; 99US-0140264.

XX 14-SEP-1999; 99US-0153872.

XX 19-NOV-1999; 99US-0166573.

XX

PA (CVTH-) CV THERAPEUTICS INC.
 PI Lawn RM, Wade D, Garvin M;
 XX WPI; 2001-137812/14.
 DR
 XX
 PT Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
 PT useful for the development of agents for the treatment of heart disease
 PT and other disorders associated with hypercholesterolemia and
 PT atherosclerosis -
 XX
 PS Disclosure; Page 122-128; 215pp; English.
 XX
 CC The present sequence encodes a human adenosine triphosphate (ATP)
 CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
 CC membranes and utilises ATP hydrolysis to transport a wide variety of
 CC substrates across the plasma membrane. ABC1 is a pivotal protein in
 CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
 CC stores. ABC1 is defective in Tangier disease, a genetic disorder
 CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
 CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
 CC useful for developing pharmaceutical agents for the treatment of heart
 CC disease and other disorders associated with hypercholesterolemia and
 CC atherosclerosis. The genes are useful for developing screening assays to
 CC screen for compounds that regulate the expression of genes associated
 CC with cholesterol transport. The genes and proteins are also useful for
 CC are also useful as diagnostic indicators of cardiovascular disease and
 CC other disorders associated with hypercholesterolemia.
 XX
 SQ Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;

Query Match 100.0%; Score 6784; DB 22; Length 10442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 291 ATGGCTTGTGGCCCTCAGCTGAGGTGCTGCTGGGAGAACCTCCTCAGTGGAGAGA 350
 QY 61 CAACATGTCAGCTGTTACTGGAAGTGGCCGCTCTATTATCTTCTCTGATCCTGATC 120
 DB 351 CAACATGTCAGCTGTTACTGGAAGTGGCCGCTCTATTATCTTCTCTGATCCTGATC 410
 QY 121 TCTGTTCCGCTGAGTACCCACCTATGACAAACATGAATGCCATTTTCCAAATAAGGCC 180
 DB 411 TCTGTTCCGCTGAGTACCCACCTATGACAAACATGAATGCCATTTTCCAAATAAGGCC 470
 QY 181 ATGGCCCTCTGCAGGAACACTTCTCTGAGGTTCAGGGGATATCTGTAATGCCAACACCCC 240
 DB 471 ATGGCCCTCTGCAGGAACACTTCTCTGAGGTTCAGGGGATATCTGTAATGCCAACACCCC 530
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 DB 591 ATTGTGGCTCGCTTCTCAGATGCTCGGAGGCTCTTTTATACGCCAGAGAGACACC 650
 QY 361 AGCATGAAGGACATCGGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 420
 DB 651 AGCATGAAGGACATCGGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA 710
 QY 421 AACTTGAAGCTTCAAGATTCTCTGAGTGCACAACTTCTCTGGTTCCTATATAC 480
 DB 711 AACTTGAAGCTTCAAGATTCTCTGAGTGCACAACTTCTCTGGTTCCTATATAC 770
 QY 481 AACCTCTCTCCCAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGCAITCTCCAC 540
 DB 771 AACCTCTCTCCCAAGTCTACTGTGGACAAGATGCTGAGGGCTGATGCAITCTCCAC 830
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 QY 601 GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTTACCAAGAGGAG 660
 DB 891 CAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTTACCAAGAGGAG 950
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Db	6471	GGCGGCCCTCTGTGGTGTCTTGATGAACCCACCACAGCATGGATCCCAAGCCCGG	6530
QY	6241	CGGTTCTTCGGAATGTGCCCTTAGCTGTGTCAGAGAGGGAGATCAGTAGTCCTTACA	6300
Db	6531	CGGTTCTTCGGAATGTGCCCTTAGCTGTGTCAGAGAGGGAGATCAGTAGTCCTTACA	6590
QY	6301	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCAC TAGGATGGCAATCATGGTCAATGGA	6360
Db	6591	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCAC TAGGATGGCAATCATGGTCAATGGA	6650
QY	6361	AGGTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGAGATGGTTATACA	6420
Db	6651	AGGTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGAGATGGTTATACA	6710
QY	6421	ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGGAAGCTGTCCAGGATTTCTTTGGGA	6480
Db	6711	ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGGAAGCTGTCCAGGATTTCTTTGGGA	6770
QY	6481	CTTTGCATTTCTCTGGAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATACCACTT	6540
Db	6771	CTTTGCATTTCTCTGGAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATACCACTT	6830
QY	6541	CCATCTTCATATCTCTCTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAACGGA	6600
Db	6831	CCATCTTCATATCTCTCTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAACGGA	6890
QY	6601	CTCCACATAGAAGACTACTCTCTTTCTCAGACAACTTGACCAAGTATTTGTGAACCTT	6660
Db	6891	CTCCACATAGAAGACTACTCTCTTTCTCAGACAACTTGACCAAGTATTTGTGAACCTT	6950
QY	6661	GCCAAGGCCAAAGTGATGATGACCACTTAAAGACCTCTCATTTACACAAAACCCAGACA	6720
Db	6951	GCCAAGGCCAAAGTGATGATGACCACTTAAAGACCTCTCATTTACACAAAACCCAGACA	7010
QY	6721	GTAGTGGAGGTTGCAGTTCTTCACATCTTTCTTACAGGATGAGAAGTGAAAAGAAAGCTAT	6780
Db	7011	GTAGTGGAGGTTGCAGTTCTTCACATCTTTCTTACAGGATGAGAAGTGAAAAGAAAGCTAT	7070
QY	6781	GTAT 5784	
Db	7071	GTAT 7074	

RESULT 2	
AAF24702	
ID	AAF24702 standard; DNA; 10442 BP.
XX	
XX	AAF24702;
XX	AC
XX	AC
DT	20-APR-2001 (first entry)
DE	
XX	Nucleotide sequence of a human ABC1 polypeptide.
XX	
KW	Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW	apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW	chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW	atherosclerosis; cholesterol transport; ss.
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FT	291..7076
FT	CDS

FT /*tag= a
XX /product= "ABCl polypeptide"
XX
XX
XX WO200078971-A2.
XX
XX 28-DEC-2000.
XX
XX
XX 16-JUN-2000; 2000WO-US16591.
XX 18-JUN-1999; 99US-0140264.
XX 14-SEP-1999; 99US-0153872.
XX 19-NOV-1999; 99US-0166573.
XX
XX (CVTH-) CV THERAPEUTICS INC.
XX (UNIW) UNIV WASHINGTON.
XX
XX Lawn RM, Wade D, Oram JF, Garvin M;
XX
XX WPI; 2001-137811/14.
XX P-PSDE; AAB31365.
XX
XX Adenosine triphosphate (ATP) binding cassette protein (ABC) 1
FT polynucleotides and polypeptides, useful for treatment of heart disease
PT and other disorders associated with hypercholesterolemia and
PT atherosclerosis -
XX
XX Claim 3; Page 117-123; 211pp; English.
XX
XX The present sequence encodes a human adenosine triphosphate (ATP)
CC binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell
CC membranes and utilises ATP hydrolysis to transport a wide variety of
CC substrates across the plasma membrane. ABC1 is a pivotal protein in
CC the apolipoprotein-mediated mobilisation of intracellular cholesterol
CC stores. ABC1 is defective in Tangier disease, a genetic disorder
CC characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is
CC localised to chromosome 9q22-9q31. The ABC1 genes and proteins are
CC useful for developing pharmaceutical agents for the treatment of heart
CC disease and other disorders associated with hypercholesterolemia and
CC atherosclerosis. The genes are useful for developing screening assays to
CC screen for compounds that regulate the expression of genes associated
CC with cholesterol transport. The genes and proteins are also useful for
CC also useful as diagnostic indicators of cardiovascular disease and
CC other disorders associated with hypercholesterolemia.
XX
XX Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other

Query Match	100.0%;	Score 6784;	DB 22;	Length 10442;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 6784;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGCGTTGTTGGCCCTCAGCTGAGCTGCTGCTGTGGAGACCTTCATCTTCAGAGAGA	60	
Db	291	ATGGCTTTTGGCCCTCAGCTGAGCTGCTGCTGTGGAGAACCTTCATCTTCAGAGAGA	350	
Qy	61	CAACATGTCAGCTGTTTACTGGAAAGTGGCCGGCCCTCTATTATCTTCCTGATCCTGATC	120	
Db	351	CAACATGTCAGCTGTTTACTGGAAAGTGGCCGGCCCTCTATTATCTTCCTGATCCTGATC	410	
Qy	121	TCGTGTCGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAGCC	180	
Db	411	TCGTGTCGGCTGAGCTACCCACCTATGAACAACATGAATGCCATTTTCCAAATAAGCC	470	
Qy	181	ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTATGCCAACAAACCCC	240	
Db	471	ATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTATGCCAACAAACCCC	530	
Qy	241	TGTTTCCGTTTACCCGACTCCTTGGGAGGCTCCCGGAGTTGTGGAAACTTTTAACAAAATCC	300	
Db	531	TGTTTCCGTTTACCCGACTCCTTGGGAGGCTCCCGGAGTTGTGGAAACTTTTAACAAAATCC	590	
Qy	301	ATTGTGGCTCGCGCTGTTTCTCAGATGCTCGGAGGCTTCTTTTATACGCCAGAAAGACACC	360	
Db	591	ATTGTGGCTCGCGCTGTTTCTCAGATGCTCGGAGGCTTCTTTTATACGCCAGAAAGACACC	650	

QY 361 AGCATGAAGGACATGCGCAAGTTCTGAGAACATTACAGCAGATTCAAGAAATCCAGGTCA 420
DB 651 AGCATGAAGGACATGCGCAAGTTCTGAGAACATTACAGCAGATTCAAGAAATCCAGGTCA 710
QY 421 AACTTGAAGCTTCAAGATTTCCTGGTGGACAATGAACCTTCTCTGGGTTCCCTATATCAC 480
DB 711 AACTTGAAGCTTCAAGATTTCCTGGTGGACAATGAACCTTCTCTGGGTTCCCTATATCAC 770
QY 481 AACTCTCTCTCCCAAGTCTACTGTGGACAAGATGCTGAGGCTGATGTCAATCTCCAC 540
DB 771 AACTCTCTCTCCCAAGTCTACTGTGGACAAGATGCTGAGGCTGATGTCAATCTCCAC 830
QY 541 AAGGTATTTTGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
DB 831 AAGGTATTTTGAAGGCTACCAAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 890
QY 601 GAAGAGATGATTCACTTGGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAGAGGAG 660
DB 891 GAAGAGATGATTCACTTGGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAGAGGAG 950
QY 661 AAATGGCTGCAGCAGAGGAGTACTTCGTTCCAAATGACATCCTGAAGCCCAATCCTG 720
DB 951 AAATGGCTGCAGCAGAGGAGTACTTCGTTCCAAATGACATCCTGAAGCCCAATCCTG 1010
QY 721 AGAACATAACTCTACATCTCCCTTCCCGAGCAAGAGGCTGGCTGAAGCCACAAAAACA 780
DB 1011 AGAACATAACTCTACATCTCCCTTCCCGAGCAAGAGGCTGGCTGAAGCCACAAAAACA 1070
QY 781 TTGCTGATAGTTTGGGACTCTGGCCAGGAGCTGTTGACGATGAGAGCTGGAGTGAC 840
DB 1071 TTGCTGATAGTTTGGGACTCTGGCCAGGAGCTGTTGACGATGAGAGCTGGAGTGAC 1130
QY 841 ATGGCAGAGAGGTGATGTTTCTGACCAATGGAACAGCTCCAGCTCTCCACCCAAATC 900
DB 1131 ATGGCAGAGAGGTGATGTTTCTGACCAATGGAACAGCTCCAGCTCTCCACCCAAATC 1190
QY 901 TACCAGGCTGTCTGATTTGCTGGGCATCCGAGGAGGGGGGCTGAAGATCAAG 960
DB 1191 TACCAGGCTGTCTGATTTGCTGGGCATCCGAGGAGGGGGGCTGAAGATCAAG 1250
QY 961 TCTCTAACTGGTATGAGGACAACAATAACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
DB 1251 TCTCTAACTGGTATGAGGACAACAATAACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1310
QY 1021 GAAGATGCTGAACCTTCTATGACACTCTACAACTCCCTTACTGCAATGATTGATGAAG 1080
DB 1311 GAAGATGCTGAACCTTCTATGACACTCTACAACTCCCTTACTGCAATGATTGATGAAG 1370
QY 1081 AATTTGGAGTCTAGTCTCTTTCCCGCAATATCTGGAAGAGCTCTGAAGCCGCTGCTCGTT 1140
DB 1371 AATTTGGAGTCTAGTCTCTTTCCCGCAATATCTGGAAGAGCTCTGAAGCCGCTGCTCGTT 1430
QY 1141 GGAAGATCTGTATACACTGACACTCOAGCCACAAAGGCAAGTCAATGGCTGAGGTGAAC 1200
DB 1431 GGAAGATCTGTATACACTGACACTCOAGCCACAAAGGCAAGTCAATGGCTGAGGTGAAC 1490
QY 1201 AAGACCTTCCAGGAATGGCTGTGTTCCATGATCTGGAAGAGGATGAGGAGGAATCCAGC 1260
DB 1491 AAGACCTTCCAGGAATGGCTGTGTTCCATGATCTGGAAGAGGATGAGGAGGAATCCAGC 1550
QY 1261 CCAAGATCTGGACCTTCATGAGGAGAACGCCAAGAAATGGACCTTGTCCGATGCTGTG 1320
DB 1551 CCAAGATCTGGACCTTCATGAGGAGAACGCCAAGAAATGGACCTTGTCCGATGCTGTG 1610
QY 1321 GACAGAGGAGACAATCACCACATTTTGGGAACAGCAGTTGATGGCTTAGATTGGACAGCC 1380
DB 1611 GACAGAGGAGACAATCACCACATTTTGGGAACAGCAGTTGATGGCTTAGATTGGACAGCC 1670
QY 1381 CAAGACATCTGGCGTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT 1440
DB 1671 CAAGACATCTGGCGTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT 1730

QY 1441 GTGTACACCTTGAGAGAAAGCTTTCAACGAGACTAACCCAGGCAATCCGGACCATATCTCGC 1500
DB 1731 GTGTACACCTTGAGAGAAAGCTTTCAACGAGACTAACCCAGGCAATCCGGACCATATCTCGC 1790
QY 1501 TTCTATGGAGTGTCTCAACCTGAACCCATAGAACCCATAGCAACAGAAAGTCTGGCTCATC 1560
DB 1791 TTCTATGGAGTGTCTCAACCTGAACCCATAGAACCCATAGCAACAGAAAGTCTGGCTCATC 1850
QY 1561 AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTCTGGCTGGTATTGTGTCTACTGGA 1620
DB 1851 AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTCTGGCTGGTATTGTGTCTACTGGA 1910
QY 1621 AATACTCCAGGCAAGTATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1680
DB 1911 AATACTCCAGGCAAGTATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1970
QY 1681 GACAATGTGGAGAGGACAAATAAATCAAGATGGGTACTGGGACCCCTGGTCTCGAGCT 1740
DB 1971 GACAATGTGGAGAGGACAAATAAATCAAGATGGGTACTGGGACCCCTGGTCTCGAGCT 2030
QY 1741 GACCCCTTTGAGGACATGCGGTACGTTCTGGGGGCTTCCGCTACTTGCAGGATGGTGG 1800
DB 2031 GACCCCTTTGAGGACATGCGGTACGTTCTGGGGGCTTCCGCTACTTGCAGGATGGTGG 2090
QY 1801 GAGCAGGCAATCATCAGGGTGTGACGGGCAACCCAGAGAAAGAACTGTGTCTATATGCAA 1860
DB 2091 GAGCAGGCAATCATCAGGGTGTGACGGGCAACCCAGAGAAAGAACTGTGTCTATATGCAA 2150
QY 1861 CAGATGCCCTATCCCTGTTAGTTGATGACATCTTCTGCGGGTCAAGCCGGTCAATG 1920
DB 2151 CAGATGCCCTATCCCTGTTAGTTGATGACATCTTCTGCGGGTCAAGCCGGTCAATG 2210
QY 1921 CCCCCTTTTCATGACCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATGGT 1980
DB 2211 CCCCCTTTTCATGACCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATGGT 2270
QY 1981 TATGAGAGGAGGACGCTGAAAGAGACCATGGGATCATGGGCTGGGCAACAGACATA 2040
DB 2271 TATGAGAGGAGGACGCTGAAAGAGACCATGGGATCATGGGCTGGGCAACAGACATA 2330
QY 2041 CTCTGTTTATGCTGTTTCAATAGTAGCCTCATCTCTCTTCTTGTGAGCCCTGGCTGCTA 2100
DB 2331 CTCTGTTTATGCTGTTTCAATAGTAGCCTCATCTCTCTTCTTGTGAGCCCTGGCTGCTA 2390
QY 2101 GTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTATCCAGCGTGGTGTGTGTC 2160
DB 2391 GTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTATCCAGCGTGGTGTGTGTC 2450
QY 2161 TTCCCTGCTCCGTGTTGCTGTGTGACAACTCTGCAGTCTCTCTGATTAGCACACTCTTC 2220
DB 2451 TTCCCTGCTCCGTGTTGCTGTGTGACAACTCTGCAGTCTCTCTGATTAGCACACTCTTC 2510
QY 2221 TCCAGAGCAACCTTGGCAGCAGCCTGTGGGGCATCATCTACTTCAGCTGTACTCTGCC 2280
DB 2511 TCCAGAGCAACCTTGGCAGCAGCCTGTGGGGCATCATCTACTTCAGCTGTACTCTGCC 2570
QY 2281 TAGCTCCCTGTGTGGCATGCAGGACTACCTGGGCTTCACACTCAAGATCTTCGCTAGC 2340
DB 2571 TAGCTCCCTGTGTGGCATGCAGGACTACCTGGGCTTCACACTCAAGATCTTCGCTAGC 2630
QY 2341 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGACAG 2400
DB 2631 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGACAG 2690
QY 2401 GGCATTTGAGTGCAGTGGGCAACCTGTTTCAGAGTCTCTGTGGAGGAGATGGCTTCAAT 2460
DB 2691 GGCATTTGAGTGCAGTGGGCAACCTGTTTCAGAGTCTCTGTGGAGGAGATGGCTTCAAT 2750
QY 2461 CTCACCACTTCGATCTCCATGATGCTGTTTTCACACTTCTCTATGGGCTGATGACCTGG 2520
DB 2751 CTCACCACTTCGATCTCCATGATGCTGTTTTCACACTTCTCTATGGGCTGATGACCTGG 2810
QY 2521 TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAAATCCAGGCCCTGTTATTTCTCTTGC 2580

Db 2811 TACATTGAGGCTGCTTTCCAGGCGCAGTACGGAAATCCAGGCCCTTGATTTTCCCTTGC 2870
 QY 2581 ACCAAGTCTTACTGTTTGGCGAGGAAAGTATGAGAAGAGCCACCTGGTTTCCAAACAG 2640
 Db 2871 ACCNAGTCTTACTGTTTGGCGAGGAAAGTATGAGAAGAGCCACCTGGTTTCCAAACAG 2930
 QY 2641 AAGAGAAATGTCAGAAATCTGCATGAGAGGAGAACCCACCTTGAAGCTGGCGGTGCC 2700
 Db 2931 AAGAGAAATGTCAGAAATCTGCATGAGAGGAGAACCCACCTTGAAGCTGGCGGTGCC 2990
 QY 2701 ATTCAAGACCTGGTAAAGCTTACCGAGATGGGATGAAGTGGCTGTCGATGCCCTGGCA 2760
 Db 2991 ATTCAAGACCTGGTAAAGCTTACCGAGATGGGATGAAGTGGCTGTCGATGCCCTGGCA 3050
 QY 2761 CTGAATTTTATGAGGGCCAGATCACCTCTTCCCTGGGGCCCAATGGAGCGGGGAGAGCG 2820
 Db 3051 CTGAATTTTATGAGGGCCAGATCACCTCTTCCCTGGGGCCCAATGGAGCGGGGAGAGCG 3110
 QY 2821 ACCACCATGCTCAATCTGACCGGTTTCCCGCCGACCTGGGACCGCTACATCTCTG 2880
 Db 3111 ACCACCATGCTCAATCTGACCGGTTTCCCGCCGACCTGGGACCGCTACATCTCTG 3170
 QY 2881 GGAAGAGACATTCGCTCTGAGATGAGCACCATCCGCGAGAACCTGGGGTCTGTCCCGAG 2940
 Db 3171 GGAAGAGACATTCGCTCTGAGATGAGCACCATCCGCGAGAACCTGGGGTCTGTCCCGAG 3230
 QY 2941 CATACGCTGCTGTTGACATGCTGACTGTCGAGACACATCTGTTCTATGCCCGCTG 3000
 Db 3231 CATACGCTGCTGTTGACATGCTGACTGTCGAGAACACATCTGTTCTATGCCCGCTG 3290
 QY 3001 AAGGGCTCTCTGAGAGACACCTGAGGGGGAGATGGAGCAGATGGCCCTGGATGTTGT 3060
 Db 3291 AAGGGCTCTCTGAGAGACACCTGAGGGGGAGATGGAGCAGATGGCCCTGGATGTTGT 3350
 QY 3061 TTGCCATCAAGCAAGTGAAGCAAAACAGCCAGCTGTCAAGTGGATGACAGAAAG 3120
 Db 3351 TTGCCATCAAGCAAGTGAAGCAAAACAGCCAGCTGTCAAGTGGATGACAGAAAG 3410
 QY 3121 CTATCTGTGGCTTGGCTTTGTCGGGGATCTAAGCTTCTCATTTGGATGAACCCACA 3180
 Db 3411 CTATCTGTGGCTTGGCTTTGTCGGGGATCTAAGCTTCTCATTTGGATGAACCCACA 3470
 QY 3181 GCTGGTGTGAGCCCTTACTCCCGAGGGGAATGAGGAGCTGCTGCTGAAATACCCACA 3240
 Db 3471 GCTGGTGTGAGCCCTTACTCCCGAGGGGAATGAGGAGCTGCTGCTGAAATACCCACA 3530
 QY 3241 GGCGGACCATTTATCTCTACACACCATGATGATGAAGCGGACCTCTGGGGACAGG 3300
 Db 3531 GGCGGACCATTTATCTCTACACACCATGATGATGAAGCGGACCTCTGGGGACAGG 3590
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 QY 3361 CAGCTGGGACAGCTACTACCTGACCTGGTCAAGAAAGATGTGGAATCCCTCCCTCAGT 3420
 Db 3651 CAGCTGGGACAGCTACTACCTGACCTGGTCAAGAAAGATGTGGAATCCCTCCCTCAGT 3710
 QY 3421 TCCTGCAGAAACAGTAGTAGCAGCTGTGTCATACCTGAAAGAGGAGGACAGTGTTCCTCAG 3480
 Db 3711 TCCTGCAGAAACAGTAGTAGCAGCTGTGTCATACCTGAAAGAGGAGGACAGTGTTCCTCAG 3770
 QY 3481 AGCAGTTCTGATGCTGGCCTGGGAGGACCATGAGATGACACAGCTGACCATCGATGTC 3540
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 QY 3541 TCTGCTATCTCCAACTCATCAGAGCATGTGCTGAGCCCGGCTGGTGGAGACATA 3600
 Db 3831 TCTGCTATCTCCAACTCATCAGAGCATGTGCTGAGCCCGGCTGGTGGAGACATA 3690
 QY 3601 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTGAAGGAGGAGCCTTTGGGAA 3660

Db 3891 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGAGCCTTTGTGGAA 3950
 QY 3661 CTCCTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3720
 Db 3951 CTCCTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 4010
 QY 3721 GAGAGCACTCTGGAGAAATATTCCTCAAGCTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3780
 Db 4011 GAGAGCACTCTGGAGAAATATTCCTCAAGCTGGCCGAAGAGAGTGGGGTGGATGCTGAG 4070
 QY 3781 ACCTCAGATGTTACCTTCCAGCAAGACGAAGCGGGCTTCCGGGGCAACAGCAGC 3840
 Db 4071 ACCTCAGATGTTACCTTCCAGCAAGACGAAGCGGGCTTCCGGGGCAACAGCAGC 4130
 QY 3841 TGTCTTCCCGCTTACCTTGAAGATGATGCTGATCAAAATGATCTGACATGACCCCA 3900
 Db 4131 TGTCTTCCCGCTTACCTTGAAGATGATGCTGATCAAAATGATCTGACATGACCCCA 4190
 QY 3901 GAATCCAGAGAGACAGACTTGTCTAGTGGGATGGATGGCAAGGGTCTTACCAAGTGA 3960
 Db 4191 GAATCCAGAGAGACAGACTTGTCTAGTGGGATGGATGGCAAGGGTCTTACCAAGTGA 4250
 QY 3961 GGCTGGAACTTACACAGACAGATTTGTGGCCCTTTTGTGGAGAGACTGCTAATGGCC 4020
 Db 4251 GGCTGGAACTTACACAGACAGATTTGTGGCCCTTTTGTGGAGAGACTGCTAATGGCC 4310
 QY 4021 AGACGGAGTCCGAAAGATTTTGTCTCAGATTTGTCTGCCAGCTGCTTTGTCTGCAAT 4080
 Db 4311 AGACGGAGTCCGAAAGATTTTGTCTCAGATTTGTCTGCCAGCTGCTTTGTCTGCAAT 4370
 QY 4081 GCCCTTGTGTTGAGCTGATGTCGCCCTTTTGGCAAGTACCCAGCTGGAACTTCAG 4140
 Db 4371 GCCCTTGTGTTGAGCTGATGTCGCCCTTTTGGCAAGTACCCAGCTGGAACTTCAG 4430
 QY 4141 CCTCGATGTACAAGCAACAGTACACATTTGTGACCAATGATGCTCTGAGGACACGGGA 4200
 Db 4431 CCTCGATGTACAAGCAACAGTACACATTTGTGACCAATGATGCTCTGAGGACACGGGA 4490
 QY 4201 ACCCTGGAACTTTAAAGCCCTTACCAGACCTCGCTCGGACCGCTGTATGAA 4260
 Db 4491 ACCCTGGAACTTTAAAGCCCTTACCAGACCTCGCTCGGACCGCTGTATGAA 4550
 QY 4261 GGAACCCCAATCCAGACACGCTTCCAGGAGGAGGAGAGTGGACCACTGCCCA 4320
 Db 4551 GGAACCCCAATCCAGACACGCTTCCAGGAGGAGGAGAGTGGACCACTGCCCA 4610
 QY 4321 GTTCCCCAGACCATCATGGACCTCTTCCAGAAATGGGAATGGACAATGCAGAACCTTCA 4380
 Db 4611 GTTCCCCAGACCATCATGGACCTCTTCCAGAAATGGGAATGGACAATGCAGAACCTTCA 4670
 QY 4381 CCTGATGCCATGTAGCAGCAGCAAAATCAAGAGATGCTGCCCTGTGTGCCCCAGGG 4440
 Db 4671 CCTGATGCCATGTAGCAGCAGCAAAATCAAGAGATGCTGCCCTGTGTGCCCCAGGG 4730
 QY 4441 GCAGGGGGCTGCCTCTCCACAAAGAAACAAACACTGACAGATATCCTTCAGGACCTG 4500
 Db 4731 GCAGGGGGCTGCCTCTCCACAAAGAAACAAACACTGACAGATATCCTTCAGGACCTG 4790
 QY 4501 ACAGGAAGAAACATTTCCGATTTATCTGGTGAAGAGATGTGTGCAGATCATAGCCAAAGC 4560
 Db 4791 ACAGGAAGAAACATTTCCGATTTATCTGGTGAAGAGATGTGTGCAGATCATAGCCAAAGC 4850
 QY 4561 TTAAGAAACAAGATCTGGGTGAATGATTTAGTATGGGGCTTTTCCCTGGGTGTCAGT 4620
 Db 4851 TTAAGAAACAAGATCTGGGTGAATGATTTAGTATGGGGCTTTTCCCTGGGTGTCAGT 4910
 QY 4621 AATACTCAAGCACTTCTCCGAGTCAAGAGTAAATGATGCCATCAACAAATGAAGAA 4680
 Db 4911 AATACTCAAGCACTTCTCCGAGTCAAGAGTAAATGATGCCATCAACAAATGAAGAA 4970
 QY 4681 CACCTAAGAGCTGGCCAAAGACAGTTCCTGAGATCGATTTCCTCAACAGCTTGGGAAGATT 4740
 Db 4971 CACCTAAGAGCTGGCCAAAGACAGTTCCTGAGATCGATTTCCTCAACAGCTTGGGAAGATT 5030

QY	4741	ATGACAGAGCTGGACACCAGAAATATATGTCAAGGTGTGGTTCAATAACAAAGGGCTGGCAT	4800
DB	5031	ATGACAGAGCTGGACACCAGAAATATGTCAAGGTGTGGTTCAATAACAAAGGGCTGGCAT	5090
QY	4801	GCAATCAGCTCTTTCTCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAG	4860
DB	5091	GCAATCAGCTCTTTCTCTGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAG	5150
QY	4861	GGAGAGAACCTTAGCCATATATGGAATTACTGCTTTCATATCATCTCCCTGATCTCACCAAG	4920
DB	5151	GGAGAGAACCTTAGCCATATATGGAATTACTGCTTTCATATCATCTCCCTGATCTCACCAAG	5210
QY	4921	CAGCAGCTCTCAGAGGTGGCTGTGATGACCAACATCAGTGGATGCTCTTGTTGTCCATCTGT	4980
DB	5211	CAGCAGCTCTCAGAGGTGGCTGTGATGACCAACATCAGTGGATGCTCTTGTTGTCCATCTGT	5270
QY	4981	GTCATCTTTGCAATGTCTTGGTCCAGCCAGCTTTGTGCTATTCTCTGATCTCCAGGAGCGG	5040
DB	5271	GTCATCTTTGCAATGTCTTGGTCCAGCCAGCTTTGTGCTATTCTCTGATCTCCAGGAGCGG	5330
QY	5041	GTCAGCAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCTACTTGGCTC	5100
DB	5331	GTCAGCAAGCAAAACACCTGCAGTTTCATCAGTGGAGTGAAGCCTGTCTACTTGGCTC	5390
QY	5101	TCATAAATTTTCTGTGGATATGTGCAATACAGTTGTCCCTGCCACATGGTCAATTATCATC	5160
DB	5391	TCATAAATTTTCTGTGGATATGTGCAATACAGTTGTCCCTGCCACATGGTCAATTATCATC	5450
QY	5161	TTCATCTGCTTCCAGCAGAAGTCCATGTGTCTCCACCAATCTGCCCTGTCTAGGCCCTT	5220
DB	5451	TTCATCTGCTTCCAGCAGAAGTCCATGTGTCTCCACCAATCTGCCCTGTCTAGGCCCTT	5510
QY	5221	CTACTTTTGTCTGATGGTGGTCAATCACACTCTCATGTACCGAGCTCCTTTGTGTGTC	5280
DB	5511	CTACTTTTGTCTGATGGTGGTCAATCACACTCTCATGTACCGAGCTCCTTTGTGTGTC	5570
QY	5281	AAGATCCCGACGACACGCTATGTGTGTCTCACAGCGTGAACCTCTTCATTGGCATTAAT	5340
DB	5571	AAGATCCCGACGACACGCTATGTGTGTCTCACAGCGTGAACCTCTTCATTGGCATTAAT	5630
QY	5341	GGCAGGTGGCCACCTTTGTCTGGAGCTGTTCACGACATAAGCTGAATAATATCAAT	5400
DB	5631	GGCAGGTGGCCACCTTTGTCTGGAGCTGTTCACGACATAAGCTGAATAATATCAAT	5690
QY	5401	GATATCTGAAGTCCGTTCTTTGATCTTCCACATTTTGGCTGGGACGAGGGCTCATC	5460
DB	5691	GATATCTGAAGTCCGTTCTTTGATCTTCCACATTTTGGCTGGGACGAGGGCTCATC	5750
QY	5461	GACATGTTGAAAACACGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAAATCCGTTT	5520
DB	5751	GACATGTTGAAAACACGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAAATCCGTTT	5810
QY	5521	GTGTCTCACCATTATCTTGGGACTTGGTGGGAGAAACCTCTTCGCATGGCCGTGGAAGG	5580
DB	5811	GTGTCTCACCATTATCTTGGGACTTGGTGGGAGAAACCTCTTCGCATGGCCGTGGAAGG	5870
QY	5581	GTGGTGTCTTCTCATTACTGCTCTGATCCAGTACAGATCTTTCATCAGGCCAGACCT	5640
DB	5871	GTGGTGTCTTCTCATTACTGCTCTGATCCAGTACAGATCTTTCATCAGGCCAGACCT	5930
QY	5641	GTAATGCAAAAGCTATCTCCTCTGAATCATCAAGATCAAGATGTGAGCGGGGAAACACAG	5700
DB	5931	GTAATGCAAAAGCTATCTCCTCTGAATCATCAAGATGTGAGCGGGGAAACACAG	5990
QY	5701	AGAAATCTTGATGGTGGAGGCCAGAAATGACATCTTTAGAAATCAAGGAGTTGACGAGATA	5760
DB	5991	AGAAATCTTGATGGTGGAGGCCAGAAATGACATCTTTAGAAATCAAGGAGTTGACGAGATA	6050
QY	5761	TATAGAGGAACGGGAAGCTGCTCTTGCACAGGATTTTGGCTGGGCATCTCCTCTGGTGA	5820
DB	6051	TATAGAGGAACGGGAAGCTGCTCTTGCACAGGATTTTGGCTGGGCATCTCCTCTGGTGA	6110

QY	5821	TGCTTTGGGCTCCTGGGAGTTAATGGGCGTGGAAAAATCATCAACTTTCAGAGTGTAAACA	5880
DB	6111	TGCTTTGGGCTCCTGGGAGTTAATGGGCGTGGAAAAATCATCAACTTTCAGAGTGTAAACA	6170
QY	5881	GGAGATACCACTGTTTACAGAGGAGATGCTTTCCTTAACAAAAATAGTATCTTTATCAAC	5940
DB	6171	GGAGATACCACTGTTTACAGAGGAGATGCTTTCCTTAACAAAAATAGTATCTTTATCAAC	6230
QY	5941	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCACAGAGCTG	6000
DB	6231	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCACAGAGCTG	6290
QY	6001	TTGACTGGGAGAGAACAGTGGAGTTCTTTGGCTTTTCAGAGGAGTCCCACAGAGAAAGAA	6060
DB	6291	TTGACTGGGAGAGAACAGTGGAGTTCTTTGGCTTTTCAGAGGAGTCCCACAGAGAAAGAA	6350
QY	6061	GTTGGCAAGGTTGGTGAAGTGGGCGATTCGGAAACTGGGCCCTCGTGAAGTATGGAGAAAAA	6120
DB	6351	GTTGGCAAGGTTGGTGAAGTGGGCGATTCGGAAACTGGGCCCTCGTGAAGTATGGAGAAAAA	6410
QY	6121	TATGCTGGTAACATATAGTGAGGCAACAACGCAAGCTCTCTACAGCCATGGCTTGTATC	6180
DB	6411	TATGCTGGTAACATATAGTGAGGCAACAACGCAAGCTCTCTACAGCCATGGCTTGTATC	6470
QY	6181	GGCGGGCTCCTGTGGGTTTCTGGATGAACCCACACAGGCATGGATCCCAAGACCCCGG	6240
DB	6471	GGCGGGCTCCTGTGGTGTCTCTGGATGAACCCACACAGGCATGGATCCCAAGACCCCGG	6530
QY	6241	CGGTTCTTGTGGAAATGTGCCCTAACTGTTGTGCAGGAGGGAGATCAGTAGTCTTACA	6300
DB	6531	CGGTTCTTGTGGAAATGTGCCCTAACTGTTGTGCAGGAGGGAGATCAGTAGTCTTACA	6590
QY	6301	TCTCATAGTAGGAAGAATGTGAAGCTCTTGCACCTAGGATGGCAATCATGCTCAATGGGA	6360
DB	6591	TCTCATAGTAGGAAGAATGTGAAGCTCTTGCACCTAGGATGGCAATCATGCTCAATGGGA	6650
QY	6361	AGGTTTCAGGTCCTTGGCAGTGCCAGCATCTTAAATAATAGTTTGGAGATGGTTATACA	6420
DB	6651	AGGTTTCAGGTCCTTGGCAGTGCCAGCATCTTAAATAATAGTTTGGAGATGGTTATACA	6710
QY	6421	ATAGTTGTACGAATAGCAGGGTCCAAACCCGACCTTGAAGCCCTGCCAGGATTTCTTTGGGA	6480
DB	6711	ATAGTTGTACGAATAGCAGGGTCCAAACCCGACCTTGAAGCCCTGCCAGGATTTCTTTGGGA	6770
QY	6481	CTTGCAATTTCTGGAAGTGTCTTAAAGAGAAACACCGGACATGCTACATACCAGCTT	6540
DB	6771	CTTGCAATTTCTGGAAGTGTCTTAAAGAGAAACACCGGACATGCTACATACCAGCTT	6830
QY	6541	CCATCTTCATTTCTTCTCGGCCAGGATATTACAGCATCTCTCCAGAGCAAAAAGCGGA	6600
DB	6831	CCATCTTCATTTCTTCTCGGCCAGGATATTACAGCATCTCTCCAGAGCAAAAAGCGGA	6890
QY	6601	CTCCACATAGAAGACATCTCTGTTTCTCAGACAAACACITTGACCAAGTATTTGTGAACITTT	6660
DB	6891	CTCCACATAGAAGACATCTCTGTTTCTCAGACAAACACITTGACCAAGTATTTGTGAACITTT	6950
QY	6661	GCCAAAGACCAAAGTGATGATGACCACCTTAAAGACCTCTCTTATACAAAAACAGACACA	6720
DB	6951	GCCAAAGACCAAAGTGATGATGACCACCTTAAAGACCTCTCTTATACAAAAACAGACACA	7010
QY	6721	GTAGTGGACGTTTGCAGTCTCTACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	6780
DB	7011	GTAGTGGACGTTTGCAGTCTCTACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT	7070

RESULT 3
AAF24685
ID AAF24685 standard; DNA; 10474 BP.
XX

AAF24685;
 20-APR-2001 (first entry)
 Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
 Human; adenosine triphosphate binding cassette protein 1; ABC1;
 apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
 chromosome 9q22-q31; heart disease; hypercholesterolemia;
 atherosclerosis; cholesterol transport; ss.
 Homo sapiens.
 Key Location/Qualifiers
 CDS 323..7108
 /*tag= a
 /product= "defective ABC1 polypeptide"
 W0200078972-A2.
 28-DEC-2000.
 16-JUN-2000; 2000WO-US16765.
 18-JUN-1999; 99US-0140264.
 14-SEP-1999; 99US-0153872.
 19-NOV-1999; 99US-0166573.
 (CVTH-) CV THERAPEUTICS INC.
 Lawn RM, Wade D, Garvin M;
 WPI; 2001-137812/14.
 Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,
 useful for the development of agents for the treatment of heart disease
 and other disorders associated with hypercholesterolemia and
 atherosclerosis -
 Disclosure; Page 148-154; 215pp; English.
 The present sequence encodes a human adenosine triphosphate (ATP)
 binding cassette protein (ABC) 1 polypeptide, and is isolated from
 a Tangier disease patient. ABC1 resides in cell membranes and utilises
 ATP hydrolysis to transport a wide variety of substrates across the
 plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated
 mobilisation of intracellular cholesterol stores. ABC1 is defective in
 Tangier disease, a genetic disorder characterised by abnormal
 HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome
 9q22-q31. The ABC1 genes and proteins are useful for developing
 pharmaceutical agents for the treatment of heart disease and other
 disorders associated with hypercholesterolemia and atherosclerosis. The
 genes are useful for developing screening assays to screen for compounds
 that regulate the expression of genes associated with cholesterol
 transport. The genes and proteins are also useful for are also useful
 as diagnostic indicators of cardiovascular disease and other disorders
 associated with hypercholesterolemia.
 Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
 Query Match 100.0%; Score 6782.4; DB 22; Length 10474;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6793; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 1 ATGGCTTTGGGCTCAGCTAGGTTGCTGCTGTGGAAGAACCTCATTTCAGAAAGA 60
 323 ATGGCTTTGGGCTCAGCTAGGTTGCTGCTGTGGAAGAACCTCATTTCAGAAAGA 382
 61 CAACATGTCAGCTGTTACTGGAAGTGGCTGCTCTATTATCTCTGATCCTGATC 120
 383 CAACATGTCAGCTGTTACTGGAAGTGGCTGCTCTATTATCTCTGATCCTGATC 442
 121 TCTGTTGGCTGAGCTACCCACCCTATGAACAACTGAATGCCATTTTCCAAATAAGCC 180

Db 443 TCTGTTGGCTGAGCTACCCACCCTATGAACAACTGAATGCCATTTTCCAAATAAGCC 502
 Qy 181 ATGGCTTTGGGCTCAGGAAACACTTCTTGGGTTAGGGGATATCTGTATGCAACACCC 240
 Db 503 ATGGCTTTGGGCTCAGGAAACACTTCTTGGGTTAGGGGATATCTGTATGCAACACCC 562
 Qy 241 TGTTCCTGTTACCGACATCCCTGGGAGGCTCCCGAGTGTGTTGAAACTTTAAACAATCC 300
 Db 563 TGTTCCTGTTACCGACATCCCTGGGAGGCTCCCGAGTGTGTTGAAACTTTAAACAATCC 622
 Qy 301 ATTGTGGCTCGCTGTTCTCAGATGCTCGAGGCTCTCTTTATACAGCCAGAAAGACACC 360
 Db 623 ATTGTGGCTCGCTGTTCTCAGATGCTCGAGGCTCTCTTTATACAGCCAGAAAGACACC 682
 Qy 361 AGCATGAAGGACATGCCGAAAGTCTGTGAGAACATTTACAGCAGATCAAGAAATCAGCTCA 420
 Db 683 AGCATGAAGGACATGCCGAAAGTCTGTGAGAACATTTACAGCAGATCAAGAAATCAGCTCA 742
 Qy 421 AACTTGAAGCTTCAAGATTTCTGTTGGACAAATGAACCTTCTCTGGTCTCTATATCAC 480
 Db 743 AACTTGAAGCTTCAAGATTTCTGTTGGACAAATGAACCTTCTCTGGTCTCTATATCAC 802
 Qy 481 AACCTCTCTCCGAAAGTCTACTGTGACAAAGATGCTGAGGGCTGATGTCATTTCTCCAC 540
 Db 803 AACCTCTCTCCGAAAGTCTACTGTGACAAAGATGCTGAGGGCTGATGTCATTTCTCCAC 862
 Qy 541 AAGGTATTTTGAAGGCTTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
 Db 863 AAGGTATTTTGAAGGCTTACCAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 922
 Qy 601 GAAGAGATGATTCAACTTTGGTGACCAAGATTTCTGAGCTTTTGGGCTTACCAAGGAG 560
 Db 923 GAAGAGATGATTCAACTTTGGTGACCAAGATTTCTGAGCTTTTGGGCTTACCAAGGAG 982
 Qy 661 AAATGGCTGACAGAGAGGAGTACTTCTGTTCCAACTGGACATCTTGAAGCAATCTCTG 720
 Db 983 AAATGGCTGACAGAGAGGAGTACTTCTGTTCCAACTGGACATCTTGAAGCAATCTCTG 1042
 Qy 721 AGACACATAAATCTACATCTCCCTTCCGAGCAAGAGGCTGGCTGAAGCCCAAAAACA 780
 Db 1043 AGACACATAAATCTACATCTCCCTTCCGAGCAAGAGGCTGGCTGAAGCCCAAAAACA 1102
 Qy 781 TTGCTGCATAGTCTTGGGACTCTGCCGAGGAGCTGTTTCAGCATGAGAGCTGGAGTAC 840
 Db 1103 TTGCTGCATAGTCTTGGGACTCTGCCGAGGAGCTGTTTCAGCATGAGAGCTGGAGTAC 1162
 Qy 841 ATGCGACAGAGGCTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCAAAATC 900
 Db 1163 ATGCGACAGAGGCTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCAAAATC 1222
 Qy 901 TACCAGGCTGTCTCGTATTGTTCTGCGGGCATCCGAGGAGGGGGGCTGAAGATCAAG 960
 Db 1223 TACCAGGCTGTCTCGTATTGTTCTGCGGGCATCCGAGGAGGGGGGCTGAAGATCAAG 1282
 Qy 961 TCTCTCACTGTTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
 Db 1283 TCTCTCACTGTTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1342
 Qy 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTCTTACTGCAATGATTTGATGAAG 1080
 Db 1343 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTCTTACTGCAATGATTTGATGAAG 1402
 Qy 1081 AATTTGGAGCTAGTCTCTTTCCGCAATATCTGAAAGCTCTTGAAGCCGCTGCTCGTT 1140
 Db 1403 AATTTGGAGCTAGTCTCTTTCCGCAATATCTGAAAGCTCTTGAAGCCGCTGCTCGTT 1462
 Qy 1141 GGAAGATCTGTTATACACTGACACTCCAGCCACAAAGCAGGTCATGGCTGAGTGAAC 1200
 Db 1463 GGAAGATCTGTTATACACTGACACTCCAGCCACAAAGCAGGTCATGGCTGAGTGAAC 1522
 Qy 1201 AAGACCTTCCAGAACTGCTGTGTTCCATGATCTGGAGGAGCATGTGGGAGGAATCAGC 1260

Db 1523 AAGACCTTCAGGAAGTGGCTGTTCATGATCTGAAGGCAATGCGGAGAACTCAGC 1582
QY 1261 CCAGAATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGAACCTTGCAGGATGCTGTG 1320
Db 1583 CCCAAGAICTGGACCTTCATGGAGAACAGCCAAAGAAATGGAACCTTGCAGGATGCTGTG 1642
QY 1321 GACAGAGGAGACAATGACCACTTTTGGAGAACAGCACTTGGATGGCTTAGATGGACAGCC 1380
Db 1643 GACAGAGGAGACAATGACCACTTTTGGAGAACAGCACTTGGATGGCTTAGATGGACAGCC 1702
QY 1381 CAAGACATCGTGGCGTTTGGCCAAAGCACCCAGAGAGATGTCAGTCCAGTAAATGGTTCT 1440
Db 1703 CAAGACATCGTGGCGTTTGGCCAAAGCACCCAGAGAGATGTCAGTCCAGTAAATGGTTCT 1762
QY 1441 GTCTACACCTGGAGAGAGCTTCAACGAGACTAACCCAGCAATCCGAGCAATATCTCGC 1500
Db 1763 GTGTACACCTGGAGAGAGCTTCAACGAGACTAACCCAGCAATCCGAGCAATATCTCGC 1822
QY 1501 TTCAATGGAGTGTCTCAACCTGAACAGCTAGAACCCATAGCAACAGAACTCTGGCTCATC 1560
Db 1823 TTCAATGGAGTGTCTCAACCTGAACAGCTAGAACCCATAGCAACAGAACTCTGGCTCATC 1882
QY 1561 ARCAAGTCCATGAGAGTGTCTGATGAGAGAGAGTCTTGGGCTGGTATGTTGTTCTACTGA 1620
Db 1883 ARCAAGTCCATGAGAGTGTCTGATGAGAGAGAGTCTTGGGCTGGTATGTTGTTCTACTGA 1942
QY 1621 ATTACTCCAGGAGCAATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACAT 1680
Db 1943 ATTACTCCAGGAGCAATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACAT 2002
QY 1681 GACATGTGGAGAGCAAAATAAATCAAGATGGTACTGGGACCCCTGGTCTCGAGCT 1740
Db 2003 GACATGTGGAGAGCAAAATAAATCAAGATGGTACTGGGACCCCTGGTCTCGAGCT 2062
QY 1741 GACCCCTTTGAGACATGGGTACGTCTGGGGGCTCTGCCTACTTCAGAGATGTTG 1800
Db 2063 GACCCCTTTGAGACATGGGTACGTCTGGGGGCTCTGCCTACTTCAGAGATGTTG 2122
QY 1801 GAGAGGCAATCATAGGTTGTGACGGCCACCGAGAGAAACTGGTCTATATGCAA 1860
Db 2123 GAGAGGCAATCATAGGTTGTGACGGCCACCGAGAGAAACTGGTCTATATGCAA 2182
QY 1861 CAGATCCCTATCCCTGTACCTTGTATGATCTTTCGGGGTATGAGCGGTCAATG 1920
Db 2183 CAGATGCCCTATCCCTGTACCTTGTATGATCTTTCGGGGTATGAGCGGTCAATG 2242
QY 1921 CCCCCTTTCATGACCTGGCCCTGGATTTACTCAGTGGGTGTGATCATCAAGGCAATCGT 1980
Db 2243 CCCCCTTTCATGACCTGGCCCTGGATTTACTCAGTGGGTGTGATCATCAAGGCAATCGT 2302
QY 1981 TATGAGAGGAGGACGGCTGAAGAGACCATGCGGATCATGGGCTGGAGCAACAGCATA 2040
Db 2303 TATGAGAGGAGGACGGCTGAAGAGACCATGCGGATCATGGGCTGGAGCAACAGCATA 2362
QY 2041 CACTGGTTAGCTGGTTTCAATAGTAGCTCAATTCCTCTTCTGTGAGCGCTGGCTGCTA 2100
Db 2363 CACTGGTTAGCTGGTTTCAATAGTAGCTCAATTCCTCTTCTGTGAGCGCTGGCTGCTA 2422
QY 2101 GTGGTCACTGAAATAGGAACCTGTGCGCTACAGTATGCCAGCGTGGTGTGTC 2160
Db 2423 GTGGTCACTGAAATAGGAACCTGTGCGCTACAGTATGCCAGCGTGGTGTGTC 2482
QY 2161 TTCCTGTCCGTGTTGTGTGTGATCTCTGAGTGCCTTCCTGATTAGCACACTCTTC 2220
Db 2483 TTCCTGTCCGTGTTGTGTGTGATCTCTGAGTGCCTTCCTGATTAGCACACTCTTC 2542
QY 2221 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCATCTACTTCACGCTTACCTGCC 2280
Db 2543 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCATCTACTTCACGCTTACCTGCC 2602
QY 2281 TACGTCCTGTGTGGCATGCGAGACTTACGTGGCTTCACACTCAAGATCTTCGCTAGC 2340
Db 2603 TACGTCCTGTGTGGCATGCGAGACTTACGTGGCTTCACACTCAAGATCTTCGCTAGC 2662

QY 2341 CPGCTGTCTCTCTGGCTTTGGGTTTGGCTGTAGTACTTTGGCTTTTGGAGAGCAG 2400
Db 2663 CTGCTGTCTCTCTGGCTTTGGGTTTGGCTGTAGTACTTTGGCTTTTGGAGAGCAG 2722
QY 2401 GGCATTGGAGTGCAGTGGGACAACCTGTTTGCAGAGTCTCTGGAGGAGAGTGGCTCAAT 2460
Db 2723 GGCATTGGAGTGCAGTGGGACAACCTGTTTGCAGAGTCTCTGGAGGAGAGTGGCTCAAT 2782
QY 2461 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCCTCTATGGGATGATCACCTGG 2520
Db 2783 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCCTCTATGGGATGATCACCTGG 2842
QY 2521 TACATTGAGGCTGTCTTTCAGGCCAGTACGGAATTCOCAGGCCCTGGTATTTTCCTTGC 2580
Db 2843 TACATTGAGGCTGTCTTTCAGGCCAGTACGGAATTCOCAGGCCCTGGTATTTTCCTTGC 2902
QY 2581 ACCAAGTCTTACTGTTTGGCGAGGAAAGTATGATGAGAGAGCCACCTGTGTCCAAACAG 2640
Db 2903 ACCAAGTCTTACTGTTTGGCGAGGAAAGTATGATGAGAGAGCCACCTGTGTCCAAACAG 2662
QY 2641 AAGAGAATGTCAGAAATCTGCATGGAGAGAGAACCCACCTTTGAAGCTGGGCGTCTCC 2700
Db 2963 AAGAGAATGTCAGAAATCTGCATGGAGAGAGAACCCACCTTTGAAGCTGGGCGTCTCC 3022
QY 2701 ATTCAAGACCTGGTAAAGTCTACCGAGATGGGATGAAGTGGCTGCGATGGCTGGCA 2760
Db 3023 ATTCAAGACCTGGTAAAGTCTACCGAGATGGGATGAAGTGGCTGCGATGGCTGGCA 3082
QY 2761 CTGAATTTTATGAGGCCAGATCACCTCTCTCTGGGCCACAAATGAGCGGGGAGAACG 2820
Db 3083 CTGAATTTTATGAGGCCAGATCACCTCTCTCTGGGCCACAAATGAGCGGGGAGAACG 3142
QY 2821 ACCACCATGTCATCTGACCGGGTGTTCCTCCCGGACCTCGGCGCACCCCTACATCTCTG 2880
Db 3143 ACCACCATGTCATCTGACCGGGTGTTCCTCCCGGACCTCGGCGCACCCCTACATCTCTG 3202
QY 2881 GGAAGAGACATTCCTCTGAGATGAGCACCACATCCGGCAGAACCTTGGGGTCTGTCCCCAG 2940
Db 3203 GGAAGAGACATTCCTCTGAGATGAGCACCACATCCGGCAGAACCTTGGGGTCTGTCCCCAG 3262
QY 2941 CATTAAGTGTCTGTGATCTGCTGCGAAGAACACATCTGGTTCTATGCCCGCTG 3000
Db 3263 CATTAAGTGTCTGTGATCTGCTGCGAAGAACACATCTGGTTCTATGCCCGCTG 3322
QY 3001 AAAGGGCTCTCTGAGAGCAGCTGAAGCGGAGATGAGCAGATGGCCCTGGATGTTGGT 3060
Db 3323 AAAGGGCTCTCTGAGAGCAGCTGAAGCGGAGATGAGCAGATGGCCCTGGATGTTGGT 3382
QY 3061 TTGCCATCAAGAGCTGAAAGCAAAACAAAGCAAGCTGTGAGTGGAAATGCAGAGAAAG 3120
Db 3383 TTGCCATCAAGAGCTGAAAGCAAAACAAAGCAAGCTGTGAGTGGAAATGCAGAGAAAG 3442
QY 3121 CTATCTGTGGCTGTGGCTTTGTGGGGGATCTAAGTGTCTTCTGATGAACCCACA 3180
Db 3443 CTATCTGTGGCTGTGGCTTTGTGGGGGATCTAAGTGTCTTCTGATGAACCCACA 3502
QY 3181 GCTGGTGTGACCCCTTACTCCCGCAGGGGAATATGGAGCTGCTGTGAAATACCCGACAA 3240
Db 3503 GCTGGTGTGACCCCTTACTCCCGCAGGGGAATATGGAGCTGCTGTGAAATACCCGACAA 3562
QY 3241 GGGCGGACCAATTTCTCTACACACCATGATGAAGCGGACCTCTCTGGGGGACAGG 3300
Db 3563 GGGCGGACCAATTTCTCTACACACCATGATGAAGCGGACCTCTCTGGGGGACAGG 3622
QY 3301 ATTGCCATCATCTCCCATGGGAAAGCTGTGCTGTGGGCTCTCTCTGTTCTGAAGAAC 3360
Db 3623 ATTGCCATCATCTCCCATGGGAAAGCTGTGCTGTGGGCTCTCTCTGTTCTGAAGAAC 3682
QY 3361 CAGCTGGGAGACAGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3420
Db 3683 CAGCTGGGAGACAGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3742

Db	5903	GTG	GTG	TCTTCTCTCATTAC	AGTGTCTTGATCCAGTACAGATTC	TTTCTATCAGGCCCCAGACCT	5966
Qy	5641	GTA	ATG	CAAAAGCTATCTCT	CTCTGTAATGATGAAGATGAAGATGT	GAGCGGGGAAAGACAG	5700
Db	5963	GTA	ATG	CAAAAGCTATCTCT	CTCTGTAATGATGAAGATGAAGATGT	GAGCGGGGAAAGACAG	6022
Qy	5701	AGA	ATTC	TCTTGATGGTGAGCC	CAGAAATGACATCTTTAGAAATCAAGGAG	TTTGACGAAGATA	5760
Db	6023	AGA	ATTC	TCTTGATGGTGAGCC	CAGAAATGACATCTTTAGAAATCAAGGAG	TTTGACGAAGATA	6082
Qy	5761	TAT	AGA	AGGAAGCGGAAGC	GTGCTGTGACAGATTTCGCTGGGCATTTC	CTCTCTGTGTGAG	5820
Db	6083	TAT	AGA	AGGAAGCGGAAGC	GTGCTGTGACAGATTTCGCTGGGCATTTC	CTCTCTGTGTGAG	6142
Qy	5821	TGCT	TTT	GGGCTCTGGGAGTT	AATGGGCTGGAAATCATCAACTTTCAAGAT	TTTAAACA	5880
Db	6143	TGCT	TTT	GGGCTCTGGGAGTT	AATGGGCTGGAAATCATCAACTTTCAAGAT	TTTAAACA	6202
Qy	5881	GGC	ATC	ACCACCTGTTAC	CAGAGGAGATGCTTCTCTTACAAAATAGTAT	CTTTATCAAC	5940
Db	6203	GGC	ATC	ACCACCTGTTAC	CAGAGGAGATGCTTCTCTTACAAAATAGTAT	CTTTATCAAC	6262
Qy	5941	ATC	CAT	GAAGTACATCAGA	ACATGGGCTACTGCCCTCAGTTTGATGCCAT	CACAGAGCTG	6000
Db	6263	ATC	CAT	GAAGTACATCAGA	ACATGGGCTACTGCCCTCAGTTTGATGCCAT	CACAGAGCTG	6322
Qy	6001	TTG	ACT	CGGAGACACACGT	GTGAGTCTTTGGCCCTTTGAGAGAGTCC	CAGAGAAGAA	6060
Db	6323	TTG	ACT	CGGAGACACACGT	GTGAGTCTTTGGCCCTTTGAGAGAGTCC	CAGAGAAGAA	6382
Qy	6061	GTT	GCA	AGGTTGGT	CAGTGGCGGATTCCGAAACTGGGCTCTG	TGAAGTATGAGAAAAA	6120
Db	6383	GTT	GCA	AGGTTGGT	CAGTGGCGGATTCCGAAACTGGGCTCTG	TGAAGTATGAGAAAAA	6442
Qy	6121	TAT	GCT	TGCTAACTATAG	TGGAGGCAACAAACGCAAGTCTCTAC	AGCCATGGCTTTTGATC	6180
Db	6443	TAT	GCT	TGCTAACTATAG	TGGAGGCAACAAACGCAAGTCTCTAC	AGCCATGGCTTTTGATC	6502
Qy	6181	GGC	GGG	CCCTCCTGT	GTGTCTTGATCAACCCACACAGGCAT	TGGATCCCAAGCCCG	6240
Db	6503	GGC	GGG	CCCTCCTGT	GTGTCTTGATCAACCCACACAGGCAT	TGGATCCCAAGCCCG	6562
Qy	6241	CGT	TTCT	TGTGAA	TGTGCCCTTAAGTGTGTCAGAGGGGAGAT	CAGTAGTGCTTACA	6300
Db	6563	CGT	TTCT	TGTGAA	TGTGCCCTTAAGTGTGTCAGAGGGGAGAT	CAGTAGTGCTTACA	6622
Qy	6301	TCT	CAT	AGTATGAAGA	ATGTGAAGCTCTTGACACTAGGATGCA	ATCATGTGTCATGCA	6360
Db	6623	TCT	CAT	AGTATGAAGA	ATGTGAAGCTCTTGACACTAGGATGCA	ATCATGTGTCATGCA	6682
Qy	6361	AGT	TC	CAGTGCCTTGG	CAGTGTCCAGCATATAAAATAGTTTGG	AGATGTTTGGAGATGTTATACA	6420
Db	6683	AGT	TC	CAGTGCCTTGG	CAGTGTCCAGCATATAAAATAGTTTGG	AGATGTTTGGAGATGTTATACA	6742
Qy	6421	AT	AGT	TGTACGAATAC	GAGGTCACACCCGACCTGAGCCTCTC	CAGGATTTCTTTGGA	6480
Db	6743	AT	AGT	TGTACGAATAC	GAGGTCACACCCGACCTGAGCCTCTC	CAGGATTTCTTTGGA	6802
Qy	6481	CTT	GCA	TTTCTCTGG	AGTGTCTTAAAGAGAAACACCGGAAC	ATGTGTACAATACCAAGTT	6540
Db	6803	CTT	GCA	TTTCTCTGG	AGTGTCTTAAAGAGAAACACCGGAAC	ATGTGTACAATACCAAGTT	6862
Qy	6541	CC	ATC	TTCAATATCT	TCTGCGCAGGATATTAGATCTCTCTC	CCAGAGCAAAAAGCA	6600
Db	6863	CC	ATC	TTCAATATCT	TCTGCGCAGGATATTAGATCTCTCTC	CCAGAGCAAAAAGCA	6922
Qy	6601	CTC	CAT	ATAGAAGACT	ACTCTGTTTCTCAGACAACACTTGC	CAACAGTATTTGTGAACTTT	6660
Db	6923	CTC	CAT	ATAGAAGACT	ACTCTGTTTCTCAGACAACACTTGC	CAACAGTATTTGTGAACTTT	6982
Qy	6661	GCC	AGG	CCCAAGTATG	ATGACCACTTAAAGACCTCTCATTTACA	AAAAACCAAGACA	6720
Db	6983	GCC	AGG	CCCAAGTATG	ATGACCACTTAAAGACCTCTCATTTACA	AAAAACCAAGACA	7042

QY	6721	GTAGTGGACGTTGCAGTCTTCACATCTTTCTACAGGATGAGAAAGTGAAGAAGCTAT	6780
DB	7043	GTAGTGGACGTTGCAGTCTTCACATCTTTCTACAGGATGAGAAAGTGAAGAAGCTAT	7100
QY	6781	GTAT	6784
DB	7103	GTAT	7106
RESULT 4			
AAAF24686			
ID	AAF24686	standard; DNA; 10474 BP.	
XX	AC	AAF24686;	
XX	DT	20-APR-2001 (first entry)	
XX	DE	Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.	
XX	KW	Human; adenosine triphosphate binding cassette protein 1; ABC1;	
KW	KW	apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;	
KW	KW	chromosome 9q22-9q31; heart disease; hypercholesterolemia;	
KW	KW	atherosclerosis; cholesterol transport; ss.	
XX	OS	Homo sapiens.	
XX	PH	Key	Location/Qualifiers
FT	FT	CDS	323..7108
FT	FT		/tag- a
FT	FT		/product= "defective ABC1 polypeptide"
XX	PN	WO200078972-A2.	
XX	PD	28-DEC-2000.	
XX	PF	16-JUN-2000; 2000WO-US16765.	
XX	PR	18-JUN-1999; 99US-0140264.	
PR	PR	14-SEP-1999; 99US-0153872.	
PR	PR	19-NOV-1999; 99US-0166573.	
XX	XX	(CVTH-) CV THERAPEUTICS INC.	
XX	PI	Lawn RM, Wade D, Garvin M;	
XX	XX	WPI; 2001-137812/14.	
XX	PT	Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide,	
PT	PT	useful for the development of agents for the treatment of heart diseases	
PT	PT	and other disorders associated with hypercholesterolemia and	
PT	PT	atherosclerosis -	
XX	XX	Disclosure; Page 170-176; 215pp; English.	
FS	XX	The present sequence encodes a human adenosine triphosphate (ATP)	
CC	CC	binding cassette protein (ABC) 1 polypeptide, and is isolated from	
CC	CC	a Tangier disease patient. ABC1 resides in cell membranes and utilises	
CC	CC	ATP hydrolysis to transport a wide variety of substrates across the	
CC	CC	plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated	
CC	CC	mobilisation of intracellular cholesterol stores. ABC1 is defective in	
CC	CC	Tangier disease, a genetic disorder characterised by abnormal	
CC	CC	HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome	
CC	CC	9q22-9q31. The ABC1 genes and proteins are useful for developing	
CC	CC	pharmaceutical agents for the treatment of heart disease and other	
CC	CC	disorders associated with hypercholesterolemia and atherosclerosis. The	
CC	CC	genes are useful for developing screening assays to screen for compound	
CC	CC	that regulate the expression of genes associated with cholesterol	
CC	CC	transport. The genes and proteins are also useful for are also useful	
CC	CC	as diagnostic indicators of cardiovascular disease and other disorders	
CC	CC	associated with hypercholesterolemia.	
XX	XX	Sequence 10474 BP:2907 A: 2304 C: 2415 G: 2844 T: 4 other:	

Query Match 100.08; Score 5782.4; DB 22; Length 10474;
 Best Local Similarity 100.08; Pred. No. 0;
 Matches 6783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 383 CAAACATGTCAGCTGTTACTGGAAGTGGCTGGCTCTCTATTTATCTTCTGATCTGATC 442
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 Db 443 TCTGTTGGCTGAGCTTACCCACCTATGAACAACATGAATGCATTTTCCAAATAAAGCC 502
 Qy 181 ATGCCCTCTGAGGAACACTTCTCTGGTTTCAGGGATATCTGTAATGCCAACACCC 240
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 Db 683 AGCATGAAGGACATCGCAAGTCTGAGAACATACAGCAGATCAAGAAATCCAGCTCA 742
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 Db 803 AACCTCTCTCCCAAGTCTACTGTGGACAGATGCTGAGGCTGATGTCATTTCTCCAC 862
 Qy 541 AAGGTATTTTGAAGCTTACAGTTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
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 QY 3301 ATTGCCATCATCTCCCATGSGAAGCTGTCTGTGTGGGCTCTCTCCCTGTCTGTAAGAAC 3360
 Db 3623 ATTGCCATCATCTCCCATGSGAAGCTGTCTGTGTGGGCTCTCTCCCTGTCTGTAAGAAC 3682
 QY 3361 CAGCTGGGAACAGCTTACTACCTTGGTCAAGAAAGATGTGGAATCTCTCCCTCAGT 3420
 Db 3683 CAGCTGGGAACAGCTTACTACCTTGGTCAAGAAAGATGTGGAATCTCTCCCTCAGT 3742
 QY 3421 TCCTGAGAAACAGTAGTAGCTGTCTATACCTGAAAGAGGACAGTGTCTCTAG 3480
 Db 3743 TCCTGAGAAACAGTAGTAGCTGTCTATACCTGAAAGAGGACAGTGTCTCTAG 3802
 QY 3481 AGCAGTCTGTATGCTGGCTGGCAGCGACCATGAGAGTGACACGTGACCATGATGTC 3540
 Db 3803 AGCAGTCTGTATGCTGGCTGGCAGCGACCATGAGAGTGACACGTGACCATGATGTC 3862
 QY 3541 TCTGCTATCTCAACCTCATCAGGAGCATGTCTGAGCCCGCTGGTGAACACATA 3600
 Db 3863 TCTGCTATCTCAACCTCATCAGGAGCATGTCTGAGCCCGCTGGTGAACACATA 3922
 QY 3601 GGCATGAGCTGACCTATGCTGCCATATGAAGCTGTAAGGAGGAGCCCTTTGTGAA 3660
 Db 3923 GGCATGAGCTGACCTATGCTGCCATATGAAGCTGTAAGGAGGAGCCCTTTGTGAA 3982
 QY 3661 CTCTTTTCATGAGATGATGACCGCTCTCAGACCTGGGCAATTTCTAGTTATGGCATCTCA 3720
 Db 3983 CTCTTTTCATGAGATGATGACCGCTCTCAGACCTGGGCAATTTCTAGTTATGGCATCTCA 4042
 QY 3721 GAGACGACCTTGAAGAAATATTCCTCAAGTGGCCGAGAGAGTGGGCTGATGCTCAG 3780
 Db 4043 GAGACGACCTTGAAGAAATATTCCTCAAGTGGCCGAGAGAGTGGGCTGATGCTCAG 4102
 QY 3781 ACCTCAGATGATGATGCTGCCACAGAGCAACAGCGGGGCTTGGGGGCAAGCAGAGC 3840
 Db 4103 ACCTCAGATGATGATGCTGCCACAGAGCAACAGCGGGGCTTGGGGGCAAGCAGAGC 4162
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 Db 4163 TGTCTTCGCGCCCTTCACTGAAGATGATGCTGCTATCCAAATGATTTCTGACATAGACCA 4222
 QY 3901 GAATCCAGAGACAGACTTCTGCTAGTGGGATGGATGGCAAGGGTCTCTACAGGTGAAA 3960
 Db 4223 GAATCCAGAGACAGACTTCTGCTAGTGGGATGGATGGCAAGGGTCTCTACAGGTGAAA 4282
 QY 3961 GGCTGGAACCTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAGAGACTGCTAATTTGCC 4020
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 QY 4021 AGACGGAGTCGGAAGGATTTTTTGTCTCAGATGCTGTGCGAGCTGTGTTGTCTGCTGATT 4080
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QY 4081 GCCTTGTGTTTTCAGCTGTGCTGACCCCTTTTGGCAAGTACCCAGCCTGGAATCTCAG 4140
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 QY 4141 CCCTGATGTACAAAGCAAGTACATTTGTCAGCAATGATGCTCCTTGAGACAGGGA 4200
 Db 4463 CCCTGATGTACAAAGCAAGTACATTTGTCAGCAATGATGCTCCTTGAGACAGGGA 4522
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 Db 4523 ACCCTGGAACTCTTAAACGCCCTTACCAAGACCCCTTCCGGACCCGCTGTATGAA 4582
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 Db 4583 GGAACCCCAATCCAGACACGCCCTTCCAGGAGGGGAGAGAGTGAACCTGCCCCA 4642
 QY 4321 GTTCCCGAGACATCATGACCTCTTCCAGAAATGGAACTGGCAATGCAGAACCTTCA 4380
 Db 4643 GTTCCCGAGACATCATGACCTCTTCCAGAAATGGAACTGGCAATGCAGAACCTTCA 4702
 QY 4381 CCTGATGCCAGTGTAGCAGGACAAATCAAGAAGATGCTGCTGTGTCTCCCGCAGG 4440
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 QY 4861 GGAGAGAACCTTAGCCATTTATGGAATTTACTGCTTCAATCATCCCTGATCTCAACAG 4920
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DB 5723 GATATCCCTGAAGTCCGCTGTGCTGCTGAGCTGTACCGCAATTAAGCTCAATTAATCAAT 5782
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DB 5843 GTCTCACCATTATCTTGGACTTGGTGGACGAAACCTCTTGGCCATGCCGTGGAAGGG 5902
QY 5581 GTGGTGTCTTCTCTACTACTTCTGATCCAGTACAGATCTTCTCATAGGCCAGACCT 5640
DB 5903 GTGGTGTCTTCTCTACTACTTCTGATCCAGTACAGATCTTCTCATAGGCCAGACCT 5962
QY 5641 GAAATGCAAGCTATCTCTCTGAATGATGAAGTGAAGTGTGAGCGGGAAGACAG 5700
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QY 5701 AGAATCTTGATGGGAGGCGCAGATGACATCTTAGAATCAAGAGTGTGACGAAGATA 5760
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DB 6263 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6322
QY 6001 TTGACTGGGAGAGACACCTGGAGTCTTTCCTTTCAGAGGAGTCCACAGAAAGAA 6060
DB 6323 TTGACTGGGAGAGACACCTGGAGTCTTTCCTTTCAGAGGAGTCCACAGAAAGAA 6382
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QY 6181 GCGGGCCCTCTGCTGCTGTTTCTGATGAACACACAGGATGATCCCAAGCCCGG 6240
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DB 6623 TCTCATAGTATGGAAGATGTGAAGCTCTTTGGCACTAGGATGGCAATCATGGTCAATGGA 6682
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DB 6803 CTTCGATTTCTGGAAGTGTCTAAAAAGAGAAACACCGGAACATGCTACATACCACTT 6862
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DB 6923 CTCCACATAGAACTACTCTGTTTCTCAGACACACTTGACCAAGTATTGTGAACCTTT 6982
QY 6661 GCCAAGGACCAAAAGTGTGATGACCACTTAAAGACCTCTCATTACACAAAACCCAGACA 6720
DB 6983 GCCAAGGACCAAAAGTGTGATGACCACTTAAAGACCTCTCATTACACAAAACCCAGACA 7042
QY 6721 GTAGTGGACGTTGCGATTTCTCAGATCTTTCTCAGAGTGAAGAAAGTGAAGCTAT 6780
DB 7043 GTAGTGGACGTTGCGATTTCTCAGATCTTTCTCAGAGTGAAGAAAGTGAAGCTAT 7102
QY 6781 GTAT 6784
DB 7103 GTAT 7106

RESULT 6
AAF24708
ID AAF24708 standard; DNA; 10474 BP.
XX AAF24708;
AC AAF24708;
XX 20-APR-2001 (first entry)
XX Nucleotide sequence of ABC1 polypeptide from Tangier disease patient.
DE Human; adenosine triphosphate binding cassette protein 1; ABC1;
KW apolipoprotein-mediated mobilisation; cholesterol; Tangier disease;
KW chromosome 9q22-9q31; heart disease; hypercholesterolemia;
KW atherosclerosis; cholesterol transport; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 323..7108
FT /*tag= a
FT /product= "defective ABC1 polypeptide"
XX WO200078971-A2.
XX 28-DEC-2000.
XX 16-JUN-2000; 2000WO-US16591.
XX 18-JUN-1999; 99JS-0140264.
XX 14-SEP-1999; 99US-0153872.
XX 19-NOV-1999; 99US-0166573.
XX (CVTH-) CV THERAPEUTICS INC.
PA

Db	1943	ATTACTCCAGGCAGCAATTGAGTGCCTCCCATCATGTCTCAAGTACAAGATCCGAATGGACATT	2002
Qy	1581	GACAATGTGGAGAGGACAAATAAAATCAAGATGGGTACTGGGACCCCTGTCTCTCGAGCT	1740
Db	2003	GACAATGTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGACCCCTGTCTCTCGAGCT	2062
Qy	1741	GACCCCTTTGAGGACAATCGGTACTCTGTGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1800
Db	2063	GACCCCTTTGAGGACAATGTGGTACGTCTGTGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	2122
Qy	1801	GAGCAGGCAATCATCAGGCTGCTGACGGGCACCGAGAGAAACTGGTGCTATATGCAA	1860
Db	2123	GAGCAGGCAATCATCAGGCTGCTGACGGGCACCGAGAGAAACTGGTGCTATATGCAA	2182
Qy	1861	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGACGCCGTCAATG	1920
Db	2183	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGACGCCGTCAATG	2242
Qy	1921	CCCTCTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGTG	1980
Db	2243	CCCTCTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGTG	2302
Qy	1981	TATGAGAAGGAGGCACGGCTGAAAGAGACCATCGGGATCATGGCCCTGGACAACAGCATA	2040
Db	2303	TATGAGAAGGAGGCACGGCTGAAAGAGACCATCGGGATCATGGCCCTGGACAACAGCATA	2362
Qy	2041	CTCTGGTTTAGCTGGTTTCATTTAGTAGCCTCATCTCCTCTTTGTGAGCGCTGGCCTGCTA	2100
Db	2363	CTCTGGTTTAGCTGGTTTCATTTAGTAGCCTCATCTCCTCTTTGTGAGCGCTGGCCTGCTA	2422
Qy	2101	GTGCTCATCTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGCACGAGCGTGGTGTTC	2160
Db	2423	GTGCTCATCTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGCACGAGCGTGGTGTTC	2482
Qy	2161	TTCTGTTCCTGTGTTGCTGTGTGTGACATTCCTTGCAGTGCCTTCCTGTATTAGCACACTTTC	2220
Db	2483	TTCTGTTCCTGTGTTGCTGTGTGTGACATTCCTTGCAGTGCCTTCCTGTATTAGCACACTTTC	2542
Qy	2221	TCCAGAGCCAACTGGCAGCAGCCGTGTGGGGGCATCATCTACTTCAAGCTGTACCTGCC	2280
Db	2543	TCCAGAGCCAACTGGCAGCAGCCGTGTGGGGGCATCATCTACTTCAAGCTGTACCTGCC	2602
Qy	2281	TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2340
Db	2603	TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2662
Qy	2341	CTGCTGTCTCCTGTGCTTTGGGTTTGCTGTGAGTACTTTGCCCTTTTGTGGAGCAG	2400
Db	2663	CTGCTGTCTCCTGTGCTTTGGGTTTGCTGTGAGTACTTTGCCCTTTTGTGGAGCAG	2722
Qy	2401	GGCAATTGGAGTGCAGTGGGACACCTGTTTGAGAGTCCCTGTGGAGAGATGGCTTCAAT	2460
Db	2723	GGCAATTGGAGTGCAGTGGGACACCTGTTTGAGAGTCCCTGTGGAGAGATGGCTTCAAT	2782
Qy	2461	CTCACCACCTTCGATCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2520
Db	2783	CTCACCACCTTCGATCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2842
Qy	2521	TACATTGAGGCTGCTTTCCAGGCCACAGTACGGAATTCACAGCCCTCGTATTTTCCTTGC	2580
Db	2843	TACATTGAGGCTGCTTTCCAGGCCACAGTACGGAATTCACAGCCCTCGTATTTTCCTTGC	2902
Qy	2581	ACCAAGTCTCTACCTGGTTTGGCGAGGAAAGTGAAGAGAGAGCCACCTGGTTCACACAG	2640
Db	2903	ACCAAGTCTCTACCTGGTTTGGCGAGGAAAGTGAAGAGAGAGCCACCTGGTTCACACAG	2962
Qy	2641	AAGAGAATGTCAGAAATCTGTCATGTGAGGAGGAACCCACCACTTGAAGCTGGGGGTGCTC	2700
Db	2963	AAGAGAATGTCAGAAATCTGTCATGTGAGGAGGAACCCACCACTTGAAGCTGGGGGTGCTC	3022
Qy	2701	ATTACAGAACCTGGTTAAAGTCTTACCAGAGATGGGATGAAGGTGGCTGTGCATGGCCTGSCA	2760

D	b	3023	ATT	CAGAACCTGGTAA	AAAGTCTTACCGAGATGGGATGAAGGTGGCTGTGATGATGGCCTGGCA	3082
Q	y	2761	CTGAATTTTATGAGG	CCAGATCACTCCTTCTCTGGCCACAATGAGGACGGGGAAGACG	2820	
D	b	3083	CTGAATTTTATGAGG	CCAGATCACTCCTTCTCTGGCCACAATGAGGACGGGGAAGACG	3142	
Q	y	2821	ACCACCATGTCAAT	CTCTGACCGGGTTGTCCCCCCGACCTCGGGCACCGCTACATCCTG	2880	
D	b	3143	ACCACCATGTCAAT	CTCTGACCGGGTTGTCCCCCCGACCTCGGGCACCGCTACATCCTG	3202	
Q	y	2881	GGAAAGACATT	CGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGCTCTGTCCCACG	2940	
D	b	3203	GGAAAGACATT	CGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGCTCTGTCCCACG	3262	
Q	y	2941	CATAAGCTGCTGTT	GTGACATGCTGTGCAAGAACACATCTGTTCTATGTCGCCGTG	3000	
D	b	3263	CATAAGCTGCTGTT	GTGACATGCTGTGCAAGAACACATCTGTTCTATGTCGCCGTG	3322	
Q	y	3001	AAAGGGCTCTCTG	AGAGACACGTGAAGCGGAGATGGACAGATGGCCCTGGATGTTGGT	3060	
D	b	3323	AAAGGGCTCTCTG	AGAGACACGTGAAGCGGAGATGGACAGATGGCCCTGGATGTTGGT	3382	
Q	y	3061	TTGCCATCAAGCA	AGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGAAATCAGAGAAAG	3120	
D	b	3383	TTGCCATCAAGCA	AGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGAAATCAGAGAAAG	3442	
Q	y	3121	CTATCTGTGGCCT	TGGCCTTGTCTGGGGATCTAAGGTTGCAATCTGATGAACCCACA	3180	
D	b	3443	CTATCTGTGGCCT	TGGCCTTGTCTGGGGATCTAAGGTTGCAATCTGATGAACCCACA	3502	
Q	y	3181	GCTGTGTGGACCC	TTACTCCCGCAGGGGAATATGGAGCTGCTCTGAAATACCGCAA	3240	
D	b	3503	GCTGTGTGGACCC	TTACTCCCGCAGGGGAATATGGAGCTGCTCTGAAATACCGCAA	3562	
Q	y	3241	GGCCGCACCATTA	TCTCTACACACCATGATGAACGGAGCTCTCGGGGACAGG	3300	
D	b	3563	GGCCGCACCATTA	TCTCTACACACCATGATGAACGGAGCTCTCGGGGACAGG	3622	
Q	y	3301	ATTGCCATCATCT	COCCATGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTCTGAAGAAC	3360	
D	b	3623	ATTGCCATCATCT	COCCATGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTCTGAAGAAC	3682	
Q	y	3361	CAGCTGGGAACAG	GGTACTACCTTGGTCAAGAAAGATGTGGAATCCTCCTCAGT	3420	
D	b	3683	CAGCTGGGAACAG	GGTACTACCTTGGTCAAGAAAGATGTGGAATCCTCCTCAGT	3742	
Q	y	3421	TCTCGCAAAACAG	TAGTAGCCTGTGTCATACCTCAAAAAGGAGACAGTGTCTCTCAG	3480	
D	b	3743	TCTCGCAAAACAG	TAGTAGCCTGTGTCATACCTCAAAAAGGAGACAGTGTCTCTCAG	3802	
Q	y	3481	AGCAGTCTGATGT	GGCCTGGGACGGACCATGAGAGTGAACCGCTGACCATCGATGTC	3540	
D	b	3803	AGCAGTCTGATGT	GGCCTGGGACGGACCATGAGAGTGAACCGCTGACCATCGATGTC	3862	
Q	y	3541	TCTGCTATCTCCA	ACCTCATCAGGAAGCATGTCTGTGAAGCCCGCTGTGGGAAGACATA	3600	
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Q	y	3601	GGGCATGAGCTGA	CCCTATGTGCTGCCATTAAGAGCTCTAAGGAGGAGCCCTTTGTGAA	3660	
D	b	3923	GGGCATGAGCTGA	CCCTATGTGCTGCCATTAAGAGCTCTAAGGAGGAGCCCTTTGTGAA	3982	
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D	b	3983	CTCTTTTCATGAG	ATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA	4042	
Q	y	3721	GAGACGACCCCTG	GGAAGAAATATTCCTCAAGGTCGGCCGAAGAGAGTGGGTGATGCTGAG	3780	
D	b	4043	GAGACGACCCCTG	GGAAGAAATATTCCTCAAGGTCGGCCGAAGAGAGTGGGTGATGCTGAG	4102	
Q	y	3781	ACCTCAGATGGT	ACTTGTCCAGAACGACAAACAGCGGGGCCCTTCGGGGACAAAGCAGAGC	3840	
D	b	4103	ACCTCAGATGGT	ACTTGTCCAGAACGACAAACAGCGGGGCCCTTCGGGGACAAAGCAGAGC	4162	

QY 3841 TGTCTTCGCCCTTCACTGAAGATGATGCTGCTGATCCAAATGATCTGACATAGACCA 3900
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QY 3901 GAATCCAGAGACAGACTTGTCTAGTGGATGGATGGCAAGGGTCTTACAGGTGAAA 3960
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DB 5003 CACCTTAAAGCTGGCCAAAGACAGTTCTCAGATCGATTTCTCAACAGCTTGGGAAGATT 5062
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DB 5063 ATGACAGACTGGACACAGAAATAATGTCAGGTGTGGTTTCAATATACAGGGTGGCAT 5122
QY 4801 GCAATCAGCTCTTCTCCTGAATGTCATCAACAAATGCCATTTCTCCGGGCCAACCTGCAAAAG 4860
DB 5123 GCAATCAGCTCTTCTCCTGAATGTCATCAACAAATGCCATTTCTCCGGGCCAACCTGCAAAAG 5182
QY 4861 GGAGAAACCCCTAGCCATTTAGGAATTAATGCTTTCAATATCCCTTGAATTCACCAAG 4920
DB 5183 GGAGAAACCCCTAGCCATTTAGGAATTAATGCTTTCAATATCCCTTGAATTCACCAAG 5242

QY 4921 CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCAGTGGATGCTCTGTGTGCTCATCTGT 4980
DB 5243 CAGCAGCTCTCAGAGTGGCTCTGATGACCAATCAGTGGATGCTCTGTGTGCTCATCTGT 5302
QY 4981 GTCATCTTTGCAATGTCTTTCGTCGCCAGCAGCTTTGCTGATTTCTGATCCAGGAGCGG 5040
DB 5303 GTCATCTTTGCAATGTCTTTCGTCGCCAGCAGCTTTGCTGATTTCTGATCCAGGAGCGG 5362
QY 5041 GTCAGCAAGCAAAACACCTTGCAGTTTCATCAGTGGAGTGAAGCTGTCTATCTACTGGCTC 5100
DB 5363 GTCAGCAAGCAAAACACCTTGCAGTTTCATCAGTGGAGTGAAGCTGTCTATCTACTGGCTC 5422
QY 5101 TCTAATTTTGTCTGGGATATGTGCAATTTAGTTGCTCCTGCCACACTGGTGCATATATCATC 5160
DB 5423 TCTAATTTTGTCTGGGATATGTGCAATTTAGTTGCTCCTGCCACACTGGTGCATATATCATC 5482
QY 5161 TTCATCTGCTTCCAGCAGAAAGTCTTATGCTCTCTCCACCAATCTGCTGTGCTAGGCCCTT 5220
DB 5483 TTCATCTGCTTCCAGCAGAAAGTCTTATGCTCTCTCCACCAATCTGCTGTGCTAGGCCCTT 5542
QY 5221 CTACTTTTGTCTGATGGTGTGCTCAATCAGTGTGCTCTCTGCTGCTGCTGTGCTGCTGCT 5280
DB 5543 CTACTTTTGTCTGATGGTGTGCTCAATCAGTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCT 5602
QY 5281 AAGATCCCAAGCAGCAGCTATGCTGCTCTCAGCAGGTGAACCTTCTCATTTGSCATTAAT 5340
DB 5603 AAGATCCCAAGCAGCAGCTATGCTGCTCTCAGCAGGTGAACCTTCTCATTTGSCATTAAT 5662
QY 5341 GGCAGCTGCTGCCACCTTTGTGCTGGAGCTTTCACCGACAAATGAAGTGAATATATCAAT 5400
DB 5663 GGCAGCTGCTGCCACCTTTGTGCTGGAGCTTTCACCGACAAATGAAGTGAATATATCAAT 5722
QY 5401 GATATCCTGAAGTCCGTTTCTTGTATCTTCCACATTTTTCGCTGGGAGAGGCTCATC 5460
DB 5723 GATATCCTGAAGTCCGTTTCTTGTATCTTCCACATTTTTCGCTGGGAGAGGCTCATC 5782
QY 5461 GACATGTTGAAAACAGCAATGGCTGATGCTTGGAAAGTTTGGGAGATATCCTTT 5520
DB 5783 GACATGTTGAAAACAGCAATGGCTGATGCTTGGAAAGTTTGGGAGATATCCTTT 5842
QY 5521 GTGTCACATTTATCTTGGGACTTGGTGGGACGAAACCTTCTGCCCATGGCCCTGGAAGG 5580
DB 5843 GTGTCACATTTATCTTGGGACTTGGTGGGACGAAACCTTCTGCCCATGGCCCTGGAAGG 5902
QY 5581 GTGGTGTCTCTCCTCATTTACTGTTCTGATCCAGTACAGATCTTCTCATGAGGCCAGACCT 5640
DB 5903 GTGGTGTCTCTCCTCATTTACTGTTCTGATCCAGTACAGATCTTCTCATGAGGCCAGACCT 5962
QY 5641 GTAAATGCAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGGGGGAAAGACAG 5700
DB 5963 GTAAATGCAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGGGGGAAAGACAG 6022
QY 5701 AGAATCTTGATGGTGGAGCCAGAAATGACATCTTGAAGATCAAGAGATGAGGAAGATA 5760
DB 6023 AGAATCTTGATGGTGGAGCCAGAAATGACATCTTGAAGATCAAGAGATGAGGAAGATA 6082
QY 5761 TATAGAAGAAAGCGGAGCCTGCTGTTGACAGATTTGGTGGGCAATTCCTCCTGGTGAG 5820
DB 6083 TATAGAAGAAAGCGGAGCCTGCTGTTGACAGATTTGGTGGGCAATTCCTCCTGGTGAG 6142
QY 5821 TGCTTTGGGCTCTGGGAGTTAATGGGCTGGAAATCATCACTTTCAAGATGTTAACA 5880
DB 6143 TGCTTTGGGCTCTGGGAGTTAATGGGCTGGAAATCATCACTTTCAAGATGTTAACA 6202
QY 5881 GGAGATACCACTTTCACAGAGAGATGCTTCTTCTTAAACAAATAAGTATCTTATCAAC 5940
DB 6203 GGAGATACCACTTTCACAGAGAGATGCTTCTTCTTAAACAAATAAGTATCTTATCAAC 6262
QY 5941 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6000
DB 6263 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6322
QY 6001 TTGACTGGGAGAAACACGCTGGAGTTCTTTTGGCTTTTGAGAGAGTCCCGAGGAAGAA 6060

Db 6323 TTGACTGGGAGAGAACACGTGGAGTCTTTTGGCCCTTTTGGAGAGAGTCCAGAGAAAGAA 6382
Qy 6061 GTTGGCAAGCTTGGTGGGCGATTCGGAACCTCGGCTCTGAGTATGAGAGAAA 6120
Db 6383 GTTGGCAAGCTTGGTGGGCGATTCGGAACCTCGGCTCTGAGTATGAGAGAAA 6442
Qy 6121 TATGCTGGTAACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
Db 6443 TATGCTGGTAACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6502
Qy 6181 GGGGGGCTCTGTGGTCTTGGATGAGAACCCACACAGGCAATGATCCCAAGCCCGG 6240
Db 6503 GGGGGGCTCTGTGGTCTTGGATGAGAACCCACACAGGCAATGATCCCAAGCCCGG 6562
Qy 6241 CGGTCTTGTGGAACTTGGCCCTTAAGTGTCTCAAGAGGGGAGATCAGTAGTCTTACA 6300
Db 6563 CGGTCTTGTGGAACTTGGCCCTTAAGTGTCTCAAGAGGGGAGATCAGTAGTCTTACA 6622
Qy 6301 TCTCATAGTATGAAGATGAGCTCTTTGCACTAGTAGTGCATCATGGTCAATGGA 6360
Db 6623 TCTCATAGTATGAAGATGAGCTCTTTGCACTAGTAGTGCATCATGGTCAATGGA 6682
Qy 6361 AGGTTCAGGTGCTTGGCAGTGTCCAGCTCTAAATAATAGTTTGGAGATGTTTATACA 6420
Db 6683 AGGTTCAGGTGCTTGGCAGTGTCCAGCTCTAAATAATAGTTTGGAGATGTTTATACA 6742
Qy 6421 ATAGTTTACGAATAGCAGGTCCAAACCCGAGCTGAAGCTGTCCAGGATTTCTTTGGA 6480
Db 6743 ATAGTTTACGAATAGCAGGTCCAAACCCGAGCTGAAGCTGTCCAGGATTTCTTTGGA 6802
Qy 6481 CTTGCATTTCTGGAAGTGTCTAAAGAGAAACACCGGAACATGCTACAAATACCACTT 6540
Db 6803 CTTGCATTTCTGGAAGTGTCTAAAGAGAAACACCGGAACATGCTACAAATACCACTT 6862
Qy 6541 CCATCTTCATTTCTTCTGCGCAGGATATCAGCATCTCTCCAGAGCAAAAAGCGA 6600
Db 6863 CCATCTTCATTTCTTCTGCGCAGGATATCAGCATCTCTCCAGAGCAAAAAGCGA 6922
Qy 6601 CTCACATAGAAGCTACTCTGTTCTCAGACACACTTGACCAAGTATTTGTAAGTTT 6660
Db 6923 CTCACATAGAAGCTACTCTGTTCTCAGACACACTTGACCAAGTATTTGTAAGTTT 6982
Qy 6661 GCCAAGACCAAAAGTATGATGACCACTTAAAGAGACCTCTCATTACACAAAACCCAGACA 6720
Db 6983 GCCAAGACCAAAAGTATGATGACCACTTAAAGAGACCTCTCATTACACAAAACCCAGACA 7042
Qy 6721 GTAGTGACGTTGAGTTCTCACAATCTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
Db 7043 GTAGTGACGTTGAGTTCTCACAATCTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 7102
Qy 6781 GTAT 6784
Db 7103 GTAT 7106

RESULT 7
AAF92835
ID AAF92835 standard; DNA: 7860 BP.
XX
AC AAF92835;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human ABC1 cDNA.
XX
KW High density lipoprotein-cholesterol; HDL-C; cardiovascular; ABC1; ss.
XX
OS Homo sapiens.
XX
PN WO200115676-A2.
XX
PD 08-MAR-2001.

XX 01-SEP-2000; 2000WO-IB01492.
PF
XX 01-SEP-1999; 99US-0151977.
PR 15-MAR-2000; 2000US-0526193.
PR 23-JUN-2000; 2000US-0213958.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
PA (XENO-) XENON GENETICS INC.
PI Hayden MR, Brooks-Wilson AR, Pimstone SN, Clee SM;
XX WPI; 2001-244356/25.
DR
XX
XX Treating a lower than normal high density lipoprotein-cholesterol
PT (HDL-C) level, a higher than normal triglyceride level, or a
PT cardiovascular disease, by administering a compound that modulates LXR-
PT or RXR-mediated transcriptional activity.
XX
XX Disclosure; Fig 2; 317pp; English.
XX
XX The present invention relates to a method for treating a patient
CC diagnosed as having a lower than normal high density
CC lipoprotein-cholesterol (HDL-C) level, a higher than normal
CC triglyceride level, or a cardiovascular disease, involving
CC administering a compound that modulates LXR- or RXR-mediated
CC transcriptional activity or ABC1 expression or activity.
CC The LXR gene product may be used in an assay to identify
CC compounds useful for the treatment of a disease or condition selected a
CC lower than normal HDL cholesterol level, a higher than normal
CC triglyceride level, and a cardiovascular disease.
XX
SQ Sequence 7860 BP; 2014 A; 1860 C; 2008 G; 1978 T; 0 other;
Query Match 99.9%; Score 6776; DB 22; Length 7860;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6779; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ATGCGCTGTGTGCTCAGCTGAGTTGCTGTGGAAGAACTCTCTCAGAGAAAGA 60
Db 75 ATGCGCTGTGTGCTCAGCTGAGTTGCTGTGGAAGAACTCTCTCAGAGAAAGA 134
Qy 61 CAAACATGTCAGCTGTACTGGAAGTGGCTGCGCTCTATTATCTCTCTGATCTGATC 120
Db 135 CAAACATGTCAGCTGTACTGGAAGTGGCTGCGCTCTATTATCTCTCTGATCTGATC 194
Qy 121 TCTGTTGCGCTGAGCTACCCACCTATGACACATGATGCAATTTTCCAAATAAGCC 180
Db 195 TCTGTTGCGCTGAGCTACCCACCTATGACACATGATGCAATTTTCCAAATAAGCC 254
Qy 181 ATGCCCTCTGCAGGAACACTTCTCTGGGTTTCAGGGGATTTATCTGTAATGCCAACACCCC 240
Db 255 ATGCCCTCTGCAGGAACACTTCTCTGGGTTTCAGGGGATTTATCTGTAATGCCAACACCCC 314
Qy 241 TGTTCCTGTTACCCGACTCTCTGGGAGGCTCCCGGAGTTGTTGGAAACCTTTACAAATCC 300
Db 315 TGTTCCTGTTACCCGACTCTCTGGGAGGCTCCCGGAGTTGTTGGAAACCTTTACAAATCC 374
Qy 301 ATGTGCTGCTGCTGTTCTCAGATGCTCGAGGCTTCTTTTATACAGCCAGAAAGACACC 360
Db 375 ATGTGCTGCTGCTGTTCTCAGATGCTCGAGGCTTCTTTTATACAGCCAGAAAGACACC 434
Qy 361 AGCATGAAGACATGCGCAAGTTCTGAGAACATTTACAGACATCAAGAAATCCAGCTCA 420
Db 435 AGCATGAAGACATGCGCAAGTTCTGAGAACATTTACAGACATCAAGAAATCCAGCTCA 494
Qy 421 AACTTGAAGCTTCAAGATTTCTGTTGGAGCAATGAAACCTTCTCTGGTTCCTGATAC 480
Db 495 AACTTGAAGCTTCAAGATTTCTGTTGGAGCAATGAAACCTTCTCTGGTTCCTGATAC 554
Qy 481 AACTTCTCTCTCCAAAGTCTACTGTGGCAAGATGCTGAGGGCTGATGTCATTTCTCCAC 540
Db 555 AACTTCTCTCTCCAAAGTCTACTGTGGCAAGATGCTGAGGGCTGATGTCATTTCTCCAC 614

QY	541	AAGCTATTTTTCGAAGGCTACCAAGTTTACATTTGCACAAGTCTGTGCAATTGGATCAAAATCA	600
DB	615	AAGGTATTTTTCGAAGGCTACCAAGTTTACATTTGCACAAGTCTGTGCAATTGGATCAAAATCA	674
QY	601	GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTTGTGGCTTACCACAAAGGAG	660
DB	675	GAAGAGATGATTCAACTTGGTGACCAAGAAGTTTCTGAGCTTTTGTGGCTTACCACAAAGGAG	734
QY	661	AAATGTCGCTGCAGCAGAGCAGGTACTTCTGTTCCACATGAGCATCCTGAGGCCAATCTGT	720
DB	735	AAATGTCGCTGCAGCAGAGCAGGTACTTCTGTTCCACATGAGCATCCTGAGGCCAATCTGT	794
QY	721	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCTGAAGCCACACAAAACA	780
DB	795	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCTGAAGCCACACAAAACA	854
QY	781	TTGCTGCATGATCTTGGGACTCTGGCCCAAGGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC	840
DB	855	TTGCTGCATGATCTTGGGACTCTGGCCCAAGGAGCTGTTTCAGCATGAGAAGCTGGAGTGAC	914
QY	841	ATGCGACAGGAGGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCTCTCCACCACCAATC	900
DB	915	ATGCGACAGGAGGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCTCTCCACCACCAATC	974
QY	901	TACCAGGCTGTCTCGTATTTGTTCGGGGCAATCCGAGGAGGGGGCTGAAGATCAAG	960
DB	975	TACCAGGCTGTCTCGTATTTGTTCGGGGCAATCCGAGGAGGGGGCTGAAGATCAAG	1034
QY	961	TCTCTCAACTGGTATGAGGACACAACTACAAGCCCTCTTTGGAGGCAATGGCAGCTGAG	1020
DB	1035	TCTCTCAACTGGTATGAGGACACAACTACAAGCCCTCTTTGGAGGCAATGGCAGCTGAG	1094
QY	1021	GAGATGCTGAAACCTCTATGACAACTCTACAACTCCTTACTGCAATGATTTGATGAAG	1080
DB	1095	GAGATGCTGAAACCTCTATGACAACTCTACAACTCCTTACTGCAATGATTTGATGAAG	1154
QY	1081	AATTTGGAGTCTAGTCTCTCTTCCGCAATTACTGGAAGCTCTGAAGCCGCTGCTGCTT	1140
DB	1155	AATTTGGAGTCTAGTCTCTCTTCCGCAATTACTGGAAGCTCTGAAGCCGCTGCTGCTT	1214
QY	1141	GGGAAGATCCTGTATACACTGACACTCCAGCCACAAGCAGGTCATGGCTGAGGTGAAC	1200
DB	1215	GGGAAGATCCTGTATACACTGACACTCCAGCCACAAGCAGGTCATGGCTGAGGTGAAC	1274
QY	1201	AAGACCTTCCAGGAATCGCTGTGTTCATGATCTGGAAGCATGTGGGAGGAATCAGC	1260
DB	1275	AAGACCTTCCAGGAATCGCTGTGTTCATGATCTGGAAGCATGTGGGAGGAATCAGC	1334
QY	1261	CCCAAGATCTGGACCTTCATGAGAGACGCCAAGAAATGGACCTTGTCCGATGCTGTTG	1320
DB	1335	CCCAAGATCTGGACCTTCATGAGAGACGCCAAGAAATGGACCTTGTCCGATGCTGTTG	1394
QY	1321	GACAGAGGACAAATCAACACTTTTGGGAACAGCAGTTGGATGCTTAGATTGGACAGCC	1380
DB	1395	GACAGAGGACAAATCAACACTTTTGGGAACAGCAGTTGGATGCTTAGATTGGACAGCC	1454
QY	1381	CAAGACATCGTGGCGTTTTTGGCCCAAGCACCAGAGGATGTCCAGTCCAGTAATGTTCT	1440
DB	1455	CAAGACATCGTGGCGTTTTTGGCCCAAGCACCAGAGGATGTCCAGTCCAGTAATGTTCT	1514
QY	1441	GTGTACACCTGGAGAGAACTTTCAACGAGACTAACCAAGGCAATCCCGAGCCATATCTCGC	1500
DB	1515	GTGTACACCTGGAGAGAACTTTCAACGAGACTAACCAAGGCAATCCCGAGCCATATCTCGC	1574
QY	1501	TTCATGGAGTGTGTCAACCTGAAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC	1560
DB	1575	TTCATGGAGTGTGTCAACCTGAAACAGCTAGAACCCATAGCAACAGAAAGTCTGGCTCATC	1634
QY	1561	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTTGTTCACTGGA	1620
DB	1635	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTTGTTCACTGGA	1694

QY	1621	ATTACTCAGGCGACGANTGAGCTGCCCCCATCATGTCAAGATACGAATCGAATGACACATT	1680
Db	1695	ATTACTCAGGCGACGANTGAGCTGCCCCCATCATGTCAAGATACGAATCGAATGACACATT	1754
QY	1681	GACAAATGTGGAGAGGACAAATAAATCAAGGATGGTACTGGACCCCTGGTCTCTCGAGCT	1740
Db	1755	GACAAATGTGGAGAGGACAAATAAATCAAGGATGGTACTGGACCCCTGGTCTCTCGAGCT	1814
QY	1741	GACCCCTTTGAGGACATGCGGTACGCTGCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1800
Db	1815	GACCCCTTTGAGGACATGCGGTACGCTGCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1874
QY	1801	GAGCAGGCAATCATCAGGTGCTTCAGGGCACCGAGCAACAAACCTGGTCTATATGCAA	1860
Db	1875	GAGCAGGCAATCATCAGGTGCTTCAGGGCACCGAGCAACAAACCTGGTCTATATGCAA	1934
QY	1861	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTCGGGGTGATGAGCGGTCAATG	1920
Db	1935	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTCGGGGTGATGAGCGGTCAATG	1994
QY	1921	CCCCTCTTCATGAGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1980
Db	1995	CCCCTCTTCATGAGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	2054
QY	1981	TATGAGAAGGAGGACACGGCTGAAGAGAGACCATCGCGATCATGGGCTGGACAACAGGATA	2040
Db	2055	TATGAGAAGGAGGACACGGCTGAAGAGAGACCATCGCGATCATGGGCTGGACAACAGGATA	2114
QY	2041	CTCTGGTTTACGTGGTTTCATTAGTAGCTCATCTCTCTTCTTGTGAGCGCTGGCGTGCCTA	2100
Db	2115	CTCTGGTTTACGTGGTTTCATTAGTAGCTCATCTCTCTTCTTGTGAGCGCTGGCGTGCCTA	2174
QY	2101	GTGTGTCATCTCGAAGTTAGAAACCTGCTGCCCTACAGTAGATCCACAGCGTGGTGTGTC	2160
Db	2175	GTGTGTCATCTCGAAGTTAGAAACCTGCTGCCCTACAGTAGATCCACAGCGTGGTGTGTC	2234
QY	2161	TTCTGTCCGTGTTTGGCTGTGGTGCACAACTCCTGCAGTGCTTCTCTGATTAGCACACTCTTC	2220
Db	2235	TTCTGTCCGTGTTTGGCTGTGGTGCACAACTCCTGCAGTGCTTCTCTGATTAGCACACTCTTC	2294
QY	2221	TCCAGAGCAACTGGCGAGCAGCGCTGTGGGGCATCATCTACTTCACGCTCTGACTCGCC	2280
Db	2295	TCCAGAGCAACTGGCGAGCAGCGCTGTGGGGCATCATCTACTTCACGCTCTGACTCGCC	2354
QY	2281	TACGCTCTGTGTGGGATGGCAGGACTACGTGGGCTTCACTCAAGATCTTCGCTAGC	2340
Db	2355	TACGCTCTGTGTGGGATGGCAGGACTACGTGGGCTTCACTCAAGATCTTCGCTAGC	2414
QY	2341	CTGCTGTCTCCTGTGCTTTTGGGTTTGCTGTGAGTACTTTGGCTTTTGGAGGACG	2400
Db	2415	CTGCTGTCTCCTGTGCTTTTGGGTTTGCTGTGAGTACTTTGGCTTTTGGAGGACG	2474
QY	2401	GGCAATGGAGTGCAGTGGGACACCTGTTTGAGAGTCTCTGGAGGAAGATGGCTTCAAT	2460
Db	2475	GGCAATGGAGTGCAGTGGGACACCTGTTTGAGAGTCTCTGGAGGAAGATGGCTTCAAT	2534
QY	2461	CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGATGACCTGG	2520
Db	2535	CTCACCACTTCGCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGATGACCTGG	2594
QY	2521	TACATTGAGGCTGCTTTCCAGCCAGTAGACGAATCCGAGGCCCTGGTATTTTCCTTGC	2580
Db	2595	TACATTGAGGCTGCTTTCCAGCCAGTAGACGAATCCGAGGCCCTGGTATTTTCCTTGC	2654
QY	2581	ACCAAGTCTCTACTGGTTTGGGAGGAAAGTGTAGAGAGCCACCTGTTTCCAAACG	2640
Db	2655	ACCAAGTCTCTACTGGTTTGGGAGGAAAGTGTAGAGAGCCACCTGTTTCCAAACG	2714
QY	2641	AAGAGAAATGCACAAATCTGCATGGAGGAGGAACCCACCTTCAGCTGGGGCTGTC	2700
Db	2715	AAGAGAAATGCACAAATCTGCATGGAGGAGGAACCCACCTTCAGCTGGGGCTGTC	2774
QY	2701	ATTACAGAACTGGTAAAGATCTACCGAGATGGGATGAAGGTGGCTGTGATGGCGCTGGCA	2760

Db 2775 ATTGAGAACTGGTAAAAGCTACCGAGATGGGATGAAGGTGGCTGTGATGGCCCTGGCA 2834
QY 2761 CTGAATTTTATGAGGGCCAGATACCTCCCTTCCTGGGCCCAATGAGCGGGGGAAGACG 2820
Db 2835 CTGAATTTTATGAGGGCCAGATACCTCCCTTCCTGGGCCCAATGAGCGGGGGAAGACG 2894
QY 2821 ACCACCATGCTCAATCTGACCGGCTGTCCCGCCGACCTCGGGCACCGCCTACATCTCTG 2880
Db 2895 ACCACCATGCTCAATCTGACCGGCTGTCCCGCCGACCTCGGGCACCGCCTACATCTCTG 2954
QY 2881 GGAAAGACATTCGGTCTCAGATGAGCAGCACCATCCGCGCAAGACCTCGGGGCTGTGCCCGAG 2940
Db 2955 GGAAAGACATTCGGTCTCAGATGAGCAGCACCATCCGCGCAAGACCTCGGGGCTGTGCCCGAG 3014
QY 2941 CATACAGTCTGTTGACATGCTGACTGTGCGAAGACACATCTGTTCTATGCCCGCTTG 3000
Db 3015 CATACAGTCTGTTGACATGCTGACTGTGCGAAGACACATCTGTTCTATGCCCGCTTG 3074
QY 3001 AAAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGCCCTGGATGTGGT 3060
Db 3075 AAAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGCCCTGGATGTGGT 3134
QY 3061 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAAGTGGAAATGCAGAGAAAG 3120
Db 3135 TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAAGTGGAAATGCAGAGAAAG 3194
QY 3121 CTATCTGTGGCCTTGSCCTTTCTCGGGGATCTAGGTTGTCTATCTGTGATGAACCCACA 3180
Db 3195 CTATCTGTGGCCTTGSCCTTTCTCGGGGATCTAGGTTGTCTATCTGTGATGAACCCACA 3254
QY 3181 GTGTGTGTGGACCTTACTCCCGCAGGGGAATATGGAGCTGTCTGTAATACCGACAAA 3240
Db 3255 GCTGTGTGGACCTTACTCCCGCAGGGGAATATGGAGCTGTCTGTAATACCGACAAA 3314
QY 3241 GCGCGCACCAATATCTCTCTACACACACATGGATGAAGCGGACGTCTCGGGGACAGG 3300
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QY 3301 ATTGCCATCATCTCCATCGGAGCTGTGTGTGGGCTCTCCCTGTCTTCTGAAGAAC 3360
Db 3375 ATTGCCATCATCTCCATCGGAGCTGTGTGTGGGCTCTCCCTGTCTTCTGAAGAAC 3434
QY 3361 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCCTCCCTCAGT 3420
Db 3435 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCCTCCCTCAGT 3494
QY 3421 TCCTGCAGAAACAGTAGTAGCAGCTGTCTACCTGAAAGAGGAGACAGTGTCTCTCAG 3480
Db 3495 TCCTGCAGAAACAGTAGTAGCAGCTGTCTACCTGAAAGAGGAGACAGTGTCTCTCAG 3554
QY 3481 AGCAGTCTCTGATGCTGGCCTGGCAGCGACCATGAGAGTGAACAGCTGACCATGCGATGTC 3540
Db 3555 AGCAGTCTCTGATGCTGGCCTGGCAGCGACCATGAGAGTGAACAGCTGACCATGCGATGTC 3614
QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTCTGGAAGCCGGCTGGTGAAGACATA 3600
Db 3615 TCTGCTATCTCCAACTCATCAGGAAGCATGTCTGGAAGCCGGCTGGTGAAGACATA 3674
QY 3601 GGGCATCAGCTGACCTATGTGTGTCATATGAAGCTGTCTGAAGGAGGAGCCCTTTGTGAA 3660
Db 3675 GGGCATCAGCTGACCTATGTGTGTCATATGAAGCTGTCTGAAGGAGGAGCCCTTTGTGAA 3734
QY 3661 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3720
Db 3735 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3794
QY 3721 GAGACGACCTGGAAGAAATATTCCTCAAGGTGGCGGAGAGAGTGGGGTGGATGCTGAG 3780
Db 3795 GAGACGACCTGGAAGAAATATTCCTCAAGGTGGCGGAGAGAGTGGGGTGGATGCTGAG 3854
QY 3781 ACCTCAGATGGTACCTTTGCCAGCAAGACGAAACAGCGCGGCCCTTCGGGGCAAGCAGAGC 3840
|||||

Db 3855 ACCTCAGATGTTACTCTGCCAGCAAGCAAGAGCGGGGCTTCGGGGCAACAGCAGC 3914
QY 3841 TGTCTTCCCGCTTCACTGAAGATGATGCTGCTGATCCAAATGATTTCTGACATAGACCCA 3900
Db 3915 TGTCTTCCCGCTTCACTGAAGATGATGCTGCTGATCCAAATGATTTCTGACATAGACCCA 3974
QY 3901 GAATCCAGAGAGACAGACTTCTCAGTGGGATGATGGCAAGGCTCTACCAAGTGA 3960
Db 3975 GAATCCAGAGAGACAGACTTCTCAGTGGGATGATGGCAAGGCTCTACCAAGTGA 4034
QY 3961 GGCTGGAACTTACACAGCAACAGTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTTGCC 4020
Db 4035 GGCTGGAACTTACACAGCAACAGTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTTGCC 4094
QY 4021 AGACGGAGCTCGGAAGAGATTTTGTCTCAGATTTGTGTCAGCTGTGTTGTCTGCAAT 4080
Db 4095 AGACGGAGCTCGGAAGAGATTTTGTCTCAGATTTGTGTCAGCTGTGTTGTCTGCAAT 4154
QY 4081 GCCCTTGTCTCAGCTGTGTCACCCCTTTGGCAAGTACCCAGCCTGGAATTTCA 4140
Db 4155 GCCCTTGTCTCAGCTGTGTCACCCCTTTGGCAAGTACCCAGCCTGGAATTTCA 4214
QY 4141 CCTTGGATGTACAGCAACAGTACACATTTGTTCAGCAATGATGCTCTGAGGACACGGGA 4200
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QY 4201 ACCCTGGAACTCTTAAACGCCCTCACCAAGACCTTGCTTCGGGACCCGCTGTATGAA 4260
Db 4275 ACCCTGGAACTCTTAAACGCCCTCACCAAGACCTTGCTTCGGGACCCGCTGTATGAA 4334
QY 4261 GAAACCCAAATCCCAAGACACGCCCTTCAGGAGGGGAGAGAGTGAACACTTGCCTCA 4320
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QY 4321 GTTCCCAAGACCATCATGAGCTCTTCCAGATGGGAATCGACAAATCGAACCCCTTCA 4380
Db 4395 GTTCCCAAGACCATCATGAGCTCTTCCAGATGGGAATCGACAAATCGAACCCCTTCA 4454
QY 4381 CTTGATGCCAGTGTAGCAGCGACAAAATCAAGAAAGATGCTGCCTGTGTCTCCCGCAGG 4440
Db 4455 CTTGATGCCAGTGTAGCAGCGACAAAATCAAGAAAGATGCTGCCTGTGTCTCCCGCAGG 4514
QY 4441 CGAGGGGGCTGCCCTCCCAAGAAACAAACAACTGCAGATATCCTTCAGGACCTG 4500
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QY 4501 ACAGGAAGAAACATTCGGAATATCTGTTGAGAGCTATGTGCAGATCATAGCCAAAAGC 4560
Db 4575 ACAGGAAGAAACATTCGGAATATCTGTTGAGAGCTATGTGCAGATCATAGCCAAAAGC 4634
QY 4561 TTAAGAACAAAGATCTGGTGAATGATTTAGTATGGGGCTTTCCCTGGGTGTCA 4620
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QY 4621 AATCTCAAGCACTTCCCTCCGAGTCAAGAAATTAATGATGCTCAAAACAAATGAAGAA 4680
Db 4695 AATCTCAAGCACTTCCCTCCGAGTCAAGAAATTAATGATGCTCAAAACAAATGAAGAA 4754
QY 4681 CACCTAAAGCTGGCAAGACAGTCTTCAGATCGATTTCTCAACAGCTTGGGAGATTT 4740
Db 4755 CACCTAAAGCTGGCAAGACAGTCTTCAGATCGATTTCTCAACAGCTTGGGAGATTT 4814
QY 4741 ATGACAGGACTGACACAGAAATTAATGCAAGGTGTGTTTCAATAACAGGGCTGGCAT 4800
Db 4815 ATGACAGGACTGACACAGAAATTAATGCAAGGTGTGTTTCAATAACAGGGCTGGCAT 4874
QY 4801 GCAATCAGCTCTTCTCCTGAATGCTCAACAAATGCCATTTCTCCGGGCCAACCTGCAAAAG 4860
Db 4875 GCAATCAGCTCTTCTCCTGAATGCTCAACAAATGCCATTTCTCCGGGCCAACCTGCAAAAG 4934
QY 4861 GGAGAGAACCTTAGCCATTTAGTATGCAATTTCTCAATCATCTCCCTGATCTCCACAG 4920
Db 4935 GGAGAGAACCTTAGCCATTTAGTATGCAATTTCTCAATCATCTCCCTGATCTCCACAG 4994
|||||

QY 4921 CAGCAGCTCTCAGAGGTGGCTCTGATGACCATAGTGGATGCTCTGCTGCTCCATCTGT 4980
 Db 4995 CAGCAGCTCTCAGAGGTGGCTCTGATGACCATAGTGGATGCTCTGCTGCTCCATCTGT 5054
 QY 4981 GTCATCTTTGCAATGCTCTGCTCCAGCAGCTTTGCTGATCTCTGATCCAGAGCGG 5040
 Db 5055 GTCATCTTTGCAATGCTCTGCTCCAGCAGCTTTGCTGATCTCTGATCCAGAGCGG 5114
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 Db 5475 GATATCCTGAAGTCCGTGCTTTGATCTCCACATTTTGGCTGGGACGAGGGCTCATC 5534
 QY 5461 GACATGGTCAAAACACGAGCAATGCTGATGCCCTGGAAAGTTTGGGAGAACTCGCTT 5520
 Db 5535 GACATGGTCAAAACACGAGCAATGCTGATGCCCTGGAAAGTTTGGGAGAACTCGCTT 5594
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 Db 6015 ATCCATGAAGTACATCAGAACATGGGTACTGCTCCTCAGTTGATGCCATCAGAGCTG 6074

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 Db 6195 TATGCTGTAATCTATGATGGAGGCAACAAAGCGAAGCTCTCTACAGCCATGGCTTTGATC 6254
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 QY 6361 AGGTTTCAGGTCCTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGGTTTACA 6420
 Db 6435 AGGTTTCAGGTCCTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGGTTTACA 6494
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 QY 6601 CTCACATAGAAGACTACTCTGTTCTCAGACAACTTGCACCAAGTATTGTTGAACTTT 6660
 Db 6675 CTCACATAGAAGACTACTCTGTTCTCAGACAACTTGCACCAAGTATTGTTGAACTTT 6734
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 QY 6721 GTAGTGGACCTTGCAGTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
 Db 6795 GTAGTGGACCTTGCAGTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6854
 QY 6781 GTAT 6784
 Db 6855 GTAT 6858

RESULT 8
 AAF83826
 ID AAF83826 standard; DNA; 7860 BP.
 XX AAF83826;
 XX AAF83826;
 DT 06-AUG-2001 (first entry)
 XX Human ABC1 nucleotide sequence.
 XX ABC1; antilipemic; cholesterol; inhibitor; low density lipoprotein;
 XX LDL; ds.
 OS Homo sapiens.
 Key Location/Qualifiers

CDS	75..3341
FT	/tag= "a
FT	/product= "partial ABC1 protein"
FT	/note= "the coding sequence continues beyond nucleotide
FT	3341, possibly till position 6860 as identified
FT	by translating the present sequence; part of the
FT	corresponding protein is missing and nucleotide
FT	3341 corresponds to the last amino acid residue
FT	(position 1089), as indicated in the
FT	specification"
XX	
PN	WO200132184-A2.
XX	
XX	10-MAY-2001.
PD	
XX	
XX	01-NOV-2000; 2000WO-US30109.
XX	
XX	01-NOV-1999; 99US-0162803.
PR	
PR	30-JUN-2000; 2000US-0215564.
XX	
XX	(WISC) WISCONSIN ALUMNI RES FOUND.
PA	
XX	
PI	Attie AD, Cook M, Gray-Keller MP, Hayden MR, Plmstone S;
PI	Brooks-Wilson A;
DR	
XX	
XX	WPI: 2001-335779/35.
DR	P-PSDB; AAB62691.
XX	
XX	New method for inhibiting cholesterol uptake in the gut comprises
PT	administration of an inhibitor of an ABC1 protein -
PT	
XX	
PS	Disclosure; Page 34-36; 41pp; English.
XX	
CC	The invention relates to a new method for inhibiting cholesterol uptake
CC	in the gut that comprises administration of an inhibitor of an ABC1
CC	protein. The method is useful for: lowering levels of LDL (low density
CC	lipoprotein) cholesterol by reducing the activity of ABC1 protein in the
CC	intestinal cells and the abundance of the ABC1 protein in the individual
CC	by inhibiting the activity of the protein; identifying drugs that can
CC	lower serum cholesterol and LDL levels comprises assaying the drug to
CC	test if it can bind to an ABC1 protein; testing LDL cholesterol lowering
CC	agents; and for modulation of ABC1 biological activity. The present
CC	sequence represents a human ABC1 nucleotide sequence.
XX	
XX	
SQ	Sequence 7860 BP; 2013 A; 1861 C; 2009 G; 1977 T; 0 other;
	Query Match 99.8%; Score 6772.8; DB 22; Length 7860;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 6777; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	1 ATGCGTTGTGGCCTCAGCTGAGGTTGCTGCTGGGAAGAACCCTACCTTCAGAGAAGA 60
Db	
	75 ATGGCTTGTGGCCTCAGCTGAGGTTGCTGCTGGGAAGAACCCTACCTTCAGAGAAGA 134
QY	61 CAACATGTCAGCNGTTACTGGAAATGCCCTGCCTCTATTATCTTCCTCATCTGATC 120
Db	
	135 CAACATGTCAGCTGCTGGAAATGCCCTGCCTCTATTATCTTCCTCATCTGATC 194
QY	121 TCCTTCGGCTGAGCTACCCACCCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 180
Db	
	195 TCTGTTCCGCTGAGCTACCCACCCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 254
QY	181 ATGCCCTCTGGAGAACACTTCCTTGCTTCAGGGGATTATCTGTAATGCCAACACCCC 240
Db	
	255 ATGCCCTCTCGAGAACACTTCCTTGCTTCAGGGGATTATCTGTAATGCCAACACCCC 314
QY	241 TGTTTCGGTTACCCGACTTCCTGGGGAGGCTCCCGAGTGTGGAAAACCTTTAAACAAATCC 300
Db	
	315 TGTTTCGGTTACCCGACTTCCTGGGGAGGCTCCCGAGTGTGGAAAACCTTTAAACAAATCC 374
QY	301 ATTGTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAACACACC 360
Db	
	375 ATTGTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAACACACC 434

QY	361	AGCATGAAGGACATCGGCAAGTTCTTGAGAACATTTACAGCAGATCAAGAAATCCAGCTCA	420
Db	435	AGCATGAAGGACATCGCAAGTTCTTGAGAACATTTACAGCAGATCAAGAAATCCAGCTCA	494
QY	421	AACCTTGAAGCTTCAAGATTTCTCGTGTGACAAATCAAAACCTTCTCTGGTTCCTATATCAC	480
Db	495	AACCTTGAAGCTTCAAGATTTCTCGTGTGACAAATCAAAACCTTCTCGTGTTCGTATCAC	554
QY	481	AACCTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCATCTCCAC	540
Db	555	AACCTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGTCATCTCCAC	614
QY	541	AAGGTATTTTTGCAAGGCTACCAAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA	600
Db	615	AAGGTATTTTTGCAAGGCTACCAAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA	674
QY	601	GAAGAGATGATTCAACTTGGTGACCAAGATTTCTGAGCTTTGTGGCTTACCAAGGAG	660
Db	675	GAAGAGATGATTCAACTTGGTGACCAAGATTTCTGAGCTTTGTGGCTTACCAAGGAG	734
QY	661	AAACTGGCTGCACGAGGCGAGTACTTCGTTCCAAACATGACATCTCTGAAGCCAAATCCGT	720
Db	735	AAACTGGCTGCACGAGGCGAGTACTTCGTTCCAAACATGACATCTCTGAAGCCAAATCCGT	794
QY	721	AGAACACTAAACTCTACATCTCCCTTCCGAGCAAGGAGTGGCTGAAGCCACAAAACA	780
Db	795	AGAACACTAAACTCTACATCTCCCTTCCGAGCAAGGAGTGGCTGAAGCCACAAAACA	854
QY	781	TTGCTGCATAGTCTTCGGGACTCTGCCGACGAGCTGTTCAGCATGAGAACTCGACTGAC	840
Db	855	TTGCTGCATAGTCTTCGGGACTCTGCCGACGAGCTGTTCAGCATGAGAACTCGACTGAC	914
QY	841	ATGCGACGAGGAGTGATGTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	900
Db	915	ATGCGACGAGGAGTGATGTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	974
QY	901	TACGAGCTGTGCTCGTATTTCTTGGGGCATCCGAGGAGGGGGGCTCAAGATCAAG	960
Db	975	TACGAGCTGTGCTCGTATTTCTTGGGGCATCCGAGGAGGGGGGCTCAAGATCAAG	1034
QY	961	TCTCTCAACTTGGTATGAGGACAACTACAAAGCCCTTTTGGAGGCAATGGCACTGAG	1020
Db	1035	TCTCTCAACTTGGTATGAGGACAACTACAAAGCCCTTTTGGAGGCAATGGCACTGAG	1094
QY	1021	GAAGATGCTGAACCTTCTATGACAACCTACAACTCCTTACTTCCATGATTGATGAAG	1080
Db	1095	GAAGATGCTGAACCTTCTATGACAACCTACAACTCCTTACTGCAATGATTGATGAAG	1154
QY	1081	AAATTTGAGTCTAGTCTCTTTTCCCGCATTTACTTGGAAAGCTCTGAAGCCGCTCTCGTT	1140
Db	1155	AAATTTGAGTCTAGTCTCTTTTCCCGCATTTACTTGGAAAGCTCTGAAGCCGCTCTCGTT	1214
QY	1141	GGGAAGATCTGTATACACTGACACTCCAGCCACAGGCAAGTCAATGGCTGAGGTGAAC	1200
Db	1215	GGGAAGATCTGTATACACTGACACTCCAGCCACAGGCAAGTCAATGGCTGAGGTGAAC	1274
QY	1201	AAGACCTTCCAGGAACCTGGCTGTGTTCATGATCTGGAAGGCATGTGGGAGGAACCTCAGC	1260
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QY	1261	CCCAGAATCTGGACCTTCAATGGAAGAACGCCAAGAAATGACCTTGTCCCGATGCTGTTG	1320
Db	1335	CCCAGAATCTGGACCTTCAATGGAAGAACGCCAAGAAATGACCTTGTCCCGATGCTGTTG	1394
QY	1321	GACAGCAGGACAAATGACACTTTTGGGAAACAGCAGTTGGATGGCTTAGATTGGACAGCC	1380
Db	1395	GACAGCAGGACAAATGACACTTTTGGGAAACAGCAGTTGGATGGCTTAGATTGGACAGCC	1454
QY	1381	CAAGACATCGTGGCGTTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT	1440
Db	1455	CAAGACATCGTGGCGTTTTTTGGCCAAAGCACCAGAGGATGTCAGTCCAGTAATGGTTCT	1514

Db 3675 GGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3734
 Qy 3661 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTTATGSCATCTCA 3720
 Db 3735 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTTATGSCATCTCA 3794
 Qy 3721 GAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAAAGAGAGTGGGTGGATGCTGAG 3780
 Db 3795 GAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAAAGAGAGTGGGTGGATGCTGAG 3854
 Qy 3781 ACCTCAGATGGTACCTTGGCAGCAAGCAAGCAAGCGGGCCTTCGGGACACAGCAGAGC 3840
 Db 3855 ACCTCAGATGGTACCTTGGCAGCAAGCAAGCAAGCGGGCCTTCGGGACACAGCAGAGC 3914
 Qy 3841 TGTCTTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTTCTGACATAGACCCA 3900
 Db 3915 TGTCTTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTTCTGACATAGACCCA 3974
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 Qy 4621 AATCTCAGACACTTCTCCAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAA 4680
 Db 4695 AATCTCAGACACTTCTCCAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAA 4754
 Qy 4681 CACCTAAGCTGGCAGGACAGTCTGCAGATCGATTTCTCAACAGCTGGGAAGATTT 4740
 Db 4755 CACCTAAGCTGGCAGGACAGTCTGCAGATCGATTTCTCAACAGCTGGGAAGATTT 4814

Qy 4741 ATGACGAGCTGGACACACAGAAATATATGTCAAGTGTGTGTTCAATAACAAGGGCTGGCAT 4800
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 Db 4875 GCAATCAGCTTTCTGTAATGTCAATACATGCAATGCAATCTCCGGGCCCAACCTGCAAAAG 4934
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QY 5821 TGCTTTGGGCTCCGGGAGTTAATGGGCTGGAAATCATCAACTTTCAAGATGTTAAACA 5880
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 QY 6001 TTGACTGGGAGAGAACACGTGGAGTCTTTCGCCCTTTTGAGAGGATCCCGAGAAAGAA 6060
 Db 6075 TTGACTGGGAGAGAACACGTGGAGTCTTTCGCCCTTTTGAGAGGATCCCGAGAAAGAA 6134
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 Db 6195 TATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6254
 QY 6181 GCGGGGCTCCTGCTGTGTTCTTCTGATGAACCCACACAGGATGATCCCAAGCCCGG 6240
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 QY 6241 CGGTTCTGTGGAATGTGCGCTTAAGTGTGTCAGAGGGGAGATCAGTAGTCTTACA 6300
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 QY 6301 TCTCATAGTATGAAGAATGTGAAGTCTTCTGACATAGGATGCAATCATGTCATGGA 6360
 Db 6375 TCTCATAGTATGAAGAATGTGAAGTCTTCTGACATAGGATGCAATCATGTCATGGA 6434
 QY 6361 AGGTTCCAGTGGCTTGGCAGTGTCCAGCATCTAAAGAAATAGGTTTGGAGATGTTTACA 6420
 Db 6435 AGGTTCCAGTGGCTTGGCAGTGTCCAGCATCTAAAGAAATAGGTTTGGAGATGTTTACA 6494
 QY 6421 ATAGTTGTACGATACAGGTTCCACCGGACCTGGAAGCTGTCCAGGATTTCTTGA 6480
 Db 6495 ATAGTTGTACGATACAGGTTCCACCGGACCTGGAAGCTGTCCAGGATTTCTTGA 6554
 QY 6481 CTGCAATTTCCCTGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACATACCACTT 6540
 Db 6555 CTGCAATTTCCCTGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACATACCACTT 6614
 QY 6541 CCATCTTCATTAATCTCTGCGGAGATATTCAGCATCTCTCCAGAGCAAAAGCGA 6600
 Db 6615 CCATCTTCATTAATCTCTGCGGAGATATTCAGCATCTCTCCAGAGCAAAAGCGA 6674
 QY 6601 CTCACATAGAGAGTACTCTCTCTCAGACACACATGACCAAGTATTTGTGAACCTT 6660
 Db 6675 CTCACATAGAGAGTACTCTCTCTCAGACACACATGACCAAGTATTTGTGAACCTT 6734
 QY 6661 GCCAGGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6720
 Db 6735 GCCAGGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6794
 QY 6721 GTAGTGGAGTGTGAGTGTCTACATCTTCTTCTACAGGATGAGAAAGTCAAGAGCTAT 6780
 Db 6795 GTAGTGGAGTGTGAGTGTCTACATCTTCTTCTACAGGATGAGAAAGTCAAGAGCTAT 6854
 QY 6781 GTAT 6784
 Db 6855 GTAT 6858
 RESULT 9
 AAD21326
 ID AAD21326 standard; DNA; 7260 BP.
 XX

AC AAD21326;
 XX DT 28-JAN-2002 (first entry)
 XX DE Human ATP binding cassette transporter 1 (ABCI) gene.
 KW Human; ATP binding cassette transporter 1; ABCI; coronary heart disease;
 KW dermatological; atherosclerosis; cardiovascular; inflammatory disease;
 KW psoriasis; lipid disorder; antibacterial; septic shock; gene therapy;
 KW immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
 OS Homo sapiens.
 XX FH Location/Qualifiers
 FT CDS 321..7106
 FT /*tag= a
 FT /product= "Human ABCI protein"
 XX PN EP1136552-A1.
 XX PD 26-SEP-2001.
 XX PF 20-MAR-2000; 2000EP-0105820.
 XX PR 20-MAR-2000; 2000EP-0105820.
 XX PA (FARB) BAYER AG.
 XX PI Schmitz G, Bodzioch M;
 XX WPI: 2001-640388/74.
 XX P-PSDB; AAE13022.
 XX New adenosine triphosphate binding cassette transporter-1 gene
 XX polymorphisms, useful for diagnosing and treating lipid disorders,
 XX cardiovascular diseases and inflammatory diseases
 XX Example 1; Fig 1; 48pp; English.

The invention relates to four common polymorphisms in the gene encoding
 ABCI-binding cassette transporter-1 (ABCI). ABCI is associated with
 decreased ApoA-1 mediated efflux of cholesterol. The polymorphisms in
 ABCI directly affects cellular lipid homeostasis, which is a key factor
 in the atherogenetic processes. The ABCI polymorphisms are useful for
 diagnosing and treating lipid disorders, cardiovascular diseases
 (coronary heart disease, atherosclerosis) and inflammatory diseases
 (psoriasis, lupus erythematosus). The identification of ABCI as a
 transporter for interleukin-beta (IL-1beta) identifies this gene as
 a candidate for treatment of inflammatory diseases including rheumatoid
 arthritis and septic shock. The present sequence is human ABCI gene.

Sequence 7260 BP; 1834 A; 1765 G; 1905 G; 1756 T; 0 other;

Query Match 99.8%; Score 6768; DB 22; Length 7260;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 6774; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGCTTTGTTGGCTCAGCTGAGTTGCTGCTGGGAAGAACCTCAGTTTCAGAAAGA 60
 Db 321 ATGCTTTGTTGGCTCAGCTGAGTTGCTGCTGGGAAGAACCTCAGTTTCAGAAAGA 380
 QY 61 CAAACATGTGAGCTGTTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 120
 Db 381 CAAACATGTGAGCTGTTTACTGGAAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 440
 QY 121 TCTGTTCCGGTGGCTACCCACCTATGACACATGATGCAATTTTCCAAATAAGCC 180
 Db 441 TCTGTTCCGGTGGCTACCCACCTATGACACATGATGCAATTTTCCAAATAAGCC 500
 QY 181 ATGCCCTCTCCAGAACACTTCTTGGGTTTCAGGGGATATCTGTATGCCAAACACCC 240
 Db 501 ATGCCCTCTCCAGAACACTTCTTGGGTTTCAGGGGATATCTGTATGCCAAACACCC 560

QY 241 TGTTCCTGTTACCGACATCCCTGGGAGGCTCCCGAGTGTGGAACTTTAAACAATCC 300
DB 561 TGTTCCTGTTACCGACATCCCTGGGAGGCTCCCGAGTGTGGAACTTTAAACAATCC 620
QY 301 AATTGGCTCGCTTCTCAGATGCTCGAGGCTCTTTTATACAGCCGAAAGACACC 360
DB 621 AATTGGCTCGCTTCTCAGATGCTCGAGGCTCTTTTATACAGCCGAAAGACACC 680
QY 361 AGCATGAGGACATCGCAAGTCTGAGACATTTACAGCAGATCAAGAAATCCAGCTCA 420
DB 681 AGCATGAGGACATCGCAAGTCTGAGACATTTACAGCAGATCAAGAAATCCAGCTCA 740
QY 421 AACTTTGAAGCTTCAAGATTTCTGGTGGCAATGAAACTTCTCTGGGTTCTGTATCAC 480
DB 741 AACTTTGAAGCTTCAAGATTTCTGGTGGCAATGAAACTTCTCTGGGTTCTGTATCAC 800
QY 481 AACCTCTCTCCCAAGTCTACTGTGACAGATGCTGAGGCTGTATCTCTCCAC 540
DB 801 AACCTCTCTCCCAAGTCTACTGTGACAGATGCTGAGGCTGTATCTCTCCAC 860
QY 541 AAGGTATTTTCAAGGCTTACAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
DB 861 AAGGTATTTTCAAGGCTTACAGTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 920
QY 601 GAAGAGATGATTAAGTGGTGACCAAGATTTCTGAGCTTTTGCGCTTACCAAGGAG 660
DB 921 GAAGAGATGATTAAGTGGTGACCAAGATTTCTGAGCTTTTGCGCTTACCAAGGAG 980
QY 661 AAGTGGCTGACGAGAGGAGTACTTCTGTCACATGGACATCCTGAAGCCATCTCTG 720
DB 981 AAGTGGCTGACGAGAGGAGTACTTCTGTCACATGGACATCCTGAAGCCATCTCTG 1040
QY 721 AGAACACTTAACTTACATCTCCCTCCGAGCAAGAGAGTGGCTGAGGCCACAAACAA 780
DB 1041 AGAACACTTAACTTACATCTCCCTCCGAGCAAGAGAGTGGCTGAGGCCACAAACAA 1100
QY 781 TTGCTCATAGTCTGGGACTCTGCCAGGAGCTGTTTCAGCATGAGAGCTGGAGTGAC 840
DB 1101 TTGCTCATAGTCTGGGACTCTGCCAGGAGCTGTTTCAGCATGAGAGCTGGAGTGAC 1160
QY 841 ATGCGAGAGAGGTGATGTTCTGACCAATGTGACAGCTCCAGTCTCCACCCAAATC 900
DB 1161 ATGCGAGAGAGGTGATGTTCTGACCAATGTGACAGCTCCAGTCTCCACCCAAATC 1220
QY 901 TACAGGCTGTCTCGTATTTCTCGGGCATCCCGAGGAGGGGCTGAAGATCAAG 960
DB 1221 TACAGGCTGTCTCGTATTTCTCGGGCATCCCGAGGAGGGGCTGAAGATCAAG 1280
QY 961 TCTCTCAACTGGTATGAGGACACAACTACAAAGCCCTTTTGGAGGCAATGSCACTGAG 1020
DB 1281 TCTCTCAACTGGTATGAGGACACAACTACAAAGCCCTTTTGGAGGCAATGSCACTGAG 1340
QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1080
DB 1341 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1400
QY 1081 AATTGGAGTCTAGTCTCTTTCCCGCATTTCTGAAAGCTCTGAAGCGCTGCTGCTTT 1140
DB 1401 AATTGGAGTCTAGTCTCTTTCCCGCATTTCTGAAAGCTCTGAAGCGCTGCTGCTTT 1460
QY 1141 GGAAGATCTGTATACACTGACATCCAGCCACAAAGCAGCTATGCTGAGGTGAAC 1200
DB 1461 GGAAGATCTGTATACACTGACATCCAGCCACAAAGCAGCTATGCTGAGGTGAAC 1520
QY 1201 AAGNCCTCCAGAACTGGCTGTCTCCATGATCTGAAAGGATGTTGGAGGAATCAGC 1260
DB 1521 AAGNCCTCCAGAACTGGCTGTCTCCATGATCTGAAAGGATGTTGGAGGAATCAGC 1580
QY 1261 CCCAAGATCTGACCTTCTATGAGAGACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1320
DB 1581 CCCAAGATCTGACCTTCTATGAGAGACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1640
QY 1321 GACAGCAGGACAAATGACCACTTTTGGGAACAGCATGGATGGCTTAGATTGGACAGCC 1380

DB 1641 GACAGCAGGACAAATGACCACTTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC 1700
QY 1381 CAAGACATCTGGGGTTTTTGGCCAAAGCACCAGAGATGTCAGATCCAGTAATGGTTCT 1440
DB 1701 CAAGACATCTGGGGTTTTTGGCCAAAGCACCAGAGATGTCAGATCCAGTAATGGTTCT 1760
QY 1441 GTGTACACCTCGGAGAGAGCTTTTCAAGGAGACTAACAGGCAATCCGAGCATAATCTCGC 1500
DB 1761 GTGTACACCTCGGAGAGAGCTTTTCAAGGAGACTAACAGGCAATCCGAGCATAATCTCGC 1820
QY 1501 TTCAATGAGTGTGTCAACCTGTAACAGCTAGAACCCATAGCAACAGAASTGTGCTCATC 1560
DB 1821 TTCAATGAGTGTGTCAACCTGTAACAGCTAGAACCCATAGCAACAGAASTGTGCTCATC 1880
QY 1561 AACAACTCCATGGAGCTGTGATGAGAGAAATTTCTGGGCTGTATTTGTGTTCACCTGGA 1620
DB 1881 AACAACTCCATGGAGCTGTGATGAGAGAAATTTCTGGGCTGTATTTGTGTTCACCTGGA 1940
QY 1621 AATTACTCAGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAAGATCCGAAATGGACAT 1880
DB 1941 AATTACTCAGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAAGATCCGAAATGGACAT 2000
QY 1681 GACAACTGGAGAGGACAAATAAATCAAGCATGGTACTGGGACCCCTGGTCTCGAGCT 1740
DB 2001 GACAACTGGAGAGGACAAATAAATCAAGCATGGTACTGGGACCCCTGGTCTCGAGCT 2060
QY 1741 GACCCCTTTGAGGACATGCGGTACTGTGGGGGCTTTCGCTACTTGTGAGGATGTGGTG 1800
DB 2061 GACCCCTTTGAGGACATGCGGTACTGTGGGGGCTTTCGCTACTTGTGAGGATGTGGTG 2120
QY 1801 GAGCAGGCAATCATCAGGCTGTGACGGCACCGAGAGAAACTGGTGTCTATATGCAA 1860
DB 2121 GAGCAGGCAATCATCAGGCTGTGACGGCACCGAGAGAAACTGGTGTCTATATGCAA 2180
QY 1861 CAGATGCCCTATCCCTGTGTAGCTTGTATGACATCTTCTCGGGGTGATGAGCCGCTCAATG 1920
DB 2181 CAGATGCCCTATCCCTGTGTAGCTTGTATGACATCTTCTCGGGGTGATGAGCCGCTCAATG 2240
QY 1921 CCCCTTTTCATGACGCTGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGATCTGTG 1980
DB 2241 CCCCTTTTCATGACGCTGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGATCTGTG 2300
QY 1981 TATGAGAGGAGGACCGGCTGAAAGAGACCATGCGGATCATCGGCTGGACAAACAGCATA 2040
DB 2301 TATGAGAGGAGGACCGGCTGAAAGAGACCATGCGGATCATCGGCTGGACAAACAGCATA 2360
QY 2041 CTCTGGTTTAGCTGTTCATTTAGTAGCCTCATCTCTTTTGTGAGCGCTGGCCTGCTA 2100
DB 2361 CTCTGGTTTAGCTGTTCATTTAGTAGCCTCATCTCTTTTGTGAGCGCTGGCCTGCTA 2420
QY 2101 GTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGTATCCAGCGTGTGTTGTC 2160
DB 2421 GTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGTATCCAGCGTGTGTTGTC 2480
QY 2161 TTCTGTCCGTTTGTGTGTGTGACAAATCTCTGAGTGTCTCTGATTTAGACACTCTTC 2220
DB 2481 TTCTGTCCGTTTGTGTGTGTGACAAATCTCTGAGTGTCTCTGATTTAGACACTCTTC 2540
QY 2221 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCTACTTACGCTGTACCTGGCC 2280
DB 2541 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCTACTTACGCTGTACCTGGCC 2600
QY 2281 TACGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCCACTCAAGATCTTCCTAGC 2340
DB 2601 TACGCTCTGTGTGGCATGGCAGGACTACGTGGGCTTCCACTCAAGATCTTCCTAGC 2660
QY 2341 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGAGAG 2400
DB 2661 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGAGAG 2720
QY 2401 GGCATTGGAGTGCAGTGGGACAACTTTTGTGAGTCTGTGGAGGAGATGGCTTCAAT 2460

QY 4621 AATACTCAAGCACTTCTCCGAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAA 4680
DB 4941 AATACTCAAGCACTTCTCCGAGTCAAGAGTTAATGATGCCACCAAAATGAAGAA 5000
QY 4681 CACCTAAAGCTGCCAAGACAGTCTCGAGATCGGATTTCTCAACACGTTGGGAAGATT 4740
DB 5001 CACCTAAAGCTGCCAAGACAGTCTCGAGATCGGATTTCTCAACACGTTGGGAAGATT 5060
QY 4741 ATGACAGGACTGGACACAGAAATAATGTCAGAGTGTGGTTCAATAACAGGCGTGGCAT 4800
DB 5061 ATGACAGGACTGGACACAGAAATAATGTCAGAGTGTGGTTCAATAACAGGCGTGGCAT 5120
QY 4801 GCAATCAGCTCTTCTCGATGTCATCAACATGCCATTCGCGGCCCAACCTGCAAAAG 4860
DB 5121 GCAATCAGCTCTTCTCGATGTCATCAACATGCCATTCGCGGCCCAACCTGCAAAAG 5180
QY 4861 GGAGAGAACCTAGCCATTAATGAATTAATGCTTTCAATCAATCCCTGATTCACCAAG 4920
DB 5181 GGAGAGAACCTAGCCATTAATGAATTAATGCTTTCAATCAATCCCTGATTCACCAAG 5240
QY 4921 CACAGCTCTCAGAGTGGCTCTGATGACACATCAGTGGATGCTGTCGTCATCTGT 4980
DB 5241 CACAGCTCTCAGAGTGGCTCTGATGACACATCAGTGGATGCTGTCGTCATCTGT 5300
QY 4981 GTCATCTTTGCAATGCTCTCCAGCCAGCTTTGTCGATTTCTGATTCACAGAGCGG 5040
DB 5301 GTCATCTTTGCAATGCTCTCCAGCCAGCTTTGTCGATTTCTGATTCACAGAGCGG 5360
QY 5041 GTCAGCAACCAACACCTGCAAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC 5100
DB 5361 GTCAGCAACCAACACCTGCAAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC 5420
QY 5101 TCTAAATTTCTCTGGGATATGCAATACGTTGTCCTGCCACATGTCATTAATCATC 5160
DB 5421 TCTAAATTTCTCTGGGATATGCAATACGTTGTCCTGCCACATGTCATTAATCATC 5480
QY 5161 TTCAATCTCTCAGCAGAGTCTCTATGTCCTCACCACATCTGCTGTGCTAGCCCTT 5220
DB 5481 TTCAATCTCTCAGCAGAGTCTCTATGTCCTCACCACATCTGCTGTGCTAGCCCTT 5540
QY 5221 CTACTTTGCTATGAGTGGTCAATCACACCTCTCATGTACCCAGCCTCTTTGTTGTC 5280
DB 5541 CTACTTTGCTATGAGTGGTCAATCACACCTCTCATGTACCCAGCCTCTTTGTTGTC 5600
QY 5281 AAGATCCCAAGCAGCCTATGTTGCTCACCAGCTGAACCTCTTCATTTGTCATTAAT 5340
DB 5601 AAGATCCCAAGCAGCCTATGTTGCTCACCAGCTGAACCTCTTCATTTGTCATTAAT 5660
QY 5341 GGCAGCTGCCACCTTTGCTGGAGCTGTTCACCGACATAGCTGAATAATATCAAT 5400
DB 5661 GGCAGCTGCCACCTTTGCTGGAGCTGTTCACCGACATAGCTGAATAATATCAAT 5720
QY 5401 GATATCCTGAAGTCCGTTCTTGAATCTCCACATTTTTCCTGGACAGGCTCATC 5460
DB 5721 GATATCCTGAAGTCCGTTCTTGAATCTCCACATTTTTCCTGGACAGGCTCATC 5780
QY 5461 GACATGTGAAAACCAAGCAATGGCTGATGCCCTGGAAGAGTTGGGAGATCGCTTT 5520
DB 5781 GACATGTGAAAACCAAGCAATGGCTGATGCCCTGGAAGAGTTGGGAGATCGCTTT 5840
QY 5521 GTGTCACCATATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGCGCGTGAAGGG 5580
DB 5841 GTGTCACCATATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGCGCGTGAAGGG 5900
QY 5581 GTGCTGTTCTTCTCAATTTACTGTTCTGATCCAGTACAGATCTTCATCAGGCCACGACT 5640
DB 5901 GTGCTGTTCTTCTCAATTTACTGTTCTGATCCAGTACAGATCTTCATCAGGCCACGACT 5960
QY 5641 GTAAATCAAGCTATCTCTCTGAATGATGAAGATGAAGTGAAGCGGGAAGACAG 5700
DB 5961 GTAAATCAAGCTATCTCTCTGAATGATGAAGATGAAGTGAAGCGGGAAGACAG 6020
QY 5701 AGAATCTTGTGAGGCGCAGATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 5760

DB 6021 AGAATCTTGTGAGTGGAGCCAGATGACATCTTAGAAATCAAGGAGTTGACGAAGATA 6080
QY 5761 TATAGAAAGAAAGCGAAGCCTGCTTTGACAGGATTTGCGTGGGCAATTCCTCCTGGTGAG 5820
DB 6081 TATAGAAAGAAAGCGAAGCCTGCTTTGACAGGATTTGCGTGGGCAATTCCTCCTGGTGAG 6140
QY 5821 TGCCTTTGGCTCCTGGAGTTAATGGGCTGAAAAATCAACATTTTCAAGATGTTAACA 5880
DB 6141 TGCCTTTGGCTCCTGGAGTTAATGGGCTGAAAAATCAACATTTTCAAGATGTTAACA 6200
QY 5881 GGAGATACCACTGTTTACCAGAGGAGATGCTTTCTTAAACAAAAATAGTATCTTATCAAC 5940
DB 6201 GGAGATACCACTGTTTACCAGAGGAGATGCTTTCTTAAACAAAAATAGTATCTTATCAAC 6260
QY 5941 ATCCATGAAGTACATCAGAACATGGCTACTGCGCTCAGTTTGTAGTCCCATCAGAGCTG 6000
DB 6261 ATCCATGAAGTACATCAGAACATGGCTACTGCGCTCAGTTTGTAGTCCCATCAGAGCTG 6320
QY 6001 TTGACTGGAGAGAACACGTCGAGTCTTTTGCCCTTTTGGAGAGGAGTCCCGAGAAAGAA 6060
DB 6321 TTGACTGGAGAGAACACGTCGAGTCTTTTGCCCTTTTGGAGAGGAGTCCCGAGAAAGAA 6380
QY 6061 GTTGGCAAGTTGTGAGTGGGCGATTCGGAACCTGGGCTCGTGAAGTATGGAGAAAAA 6120
DB 6381 GTTGGCAAGTTGTGAGTGGGCGATTCGGAACCTGGGCTCGTGAAGTATGGAGAAAAA 6440
QY 6121 TATGCTGGTAACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGCTTTGATC 6180
DB 6441 TATGCTGGTAACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGCTTTGATC 6500
QY 6181 GCGGCGCTCTGCTGTGTTCTGGATGAACCCACACAGGATGGATCCCAAGCCCGG 6240
DB 6501 GCGGCGCTCTGCTGTGTTCTGGATGAACCCACACAGGATGGATCCCAAGCCCGG 6560
QY 6241 CGGTTCTTGGAAATGTCCTTACTGTTGTCAAGAGGGGAGATCAGTAGTGTCTTACA 6300
DB 6561 CGGTTCTTGGAAATGTCCTTACTGTTGTCAAGAGGGGAGATCAGTAGTGTCTTACA 6620
QY 6301 TCTCATGATGGAAGAATGTGAAGCTCTTTCACCTAGGATGGCAATCATGTCATGA 6360
DB 6621 TCTCATGATGGAAGAATGTGAAGCTCTTTCACCTAGGATGGCAATCATGTCATGA 6680
QY 6361 AGGTTCAGTGTCTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGTTATACA 6420
DB 6681 AGGTTCAGTGTCTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGATGTTATACA 6740
QY 6421 ATAGTTGTACGATAGCAGGGTCCAAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGA 6480
DB 6741 ATAGTTGTACGATAGCAGGGTCCAAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGA 6800
QY 6481 CTTGCAATTTCTGGAGTGTCTTAAAGAGAAACACCCGGAACATGCTACAAATACGACTT 6540
DB 6801 CTTGCAATTTCTGGAGTGTCTTAAAGAGAAACACCCGGAACATGCTACAAATACGACTT 6600
QY 6541 CCATCTTCAATTTCTTCTGGCAGGATTTCCAGCATCCTCTCCAGAGCAAAAAAGCGA 6600
DB 6801 CCATCTTCAATTTCTTCTGGCAGGATTTCCAGCATCCTCTCCAGAGCAAAAAAGCGA 6920
QY 6601 CTCACATAGAAGACTACTCTGTTTCTCAGACAACTCTGACCAAGTATTTGTCGACTTT 6660
DB 6921 CTCACATAGAAGACTACTCTGTTTCTCAGACAACTCTGACCAAGTATTTGTCGACTTT 6980
QY 6661 GCCAAGGACCAAGTATGATGATGACCACTTAAAAAGCCTCTCTTACACAAAAACCCAGACA 6720
DB 6981 GCCAAGGACCAAGTATGATGATGACCACTTAAAAAGCCTCTCTTACACAAAAACCCAGACA 7040
QY 6721 GTAGTGGACGCTTGCAGTCTTCTACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
DB 7041 GTAGTGGACGCTTGCAGTCTTCTACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 7100
QY 6781 GTAT 6784
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QY 841 ATGCGACAGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 900
DB 1161 ATGGGACAGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC 1220
QY 901 TACCAGGCTGTCTCGTATTGCTGTGGGGCATCCCGAGGAGGGGGCTGAGATCAAG 960
DB 1221 TACCAGGCTGTCTCGTATTGCTGTGGGGCATCCCGAGGAGGGGGCTGAGATCAAG 1280
QY 961 TCTCTCACTGTGTATGAGGACAACTACAAAGCCCTTTTGGAGGCAATGGCACTGAG 1020
DB 1281 TCTCTCACTGTGTATGAGGACAACTACAAAGCCCTTTTGGAGGCAATGGCACTGAG 1340
QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAATCTCTTACTGCAATGATTTGATGAAG 1080
DB 1341 GAAGATGCTGAACCTTCTATGACAACTCTACAATCTCTTACTGCAATGATTTGATGAAG 1400
QY 1081 AATTGGAGTCTAGTCTCTTCCGCCATTATCTGGAAGCTCTGAAGCCGCTGCTCGTT 1140
DB 1401 AATTGGAGTCTAGTCTCTTCCGCCATTATCTGGAAGCTCTGAAGCCGCTGCTCGTT 1460
QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACAAAGCAGGTCAATGGCTGAGGTGAAC 1200
DB 1461 GGAAGATCCTGTATACACTGACACTCCAGCCACAAAGCAGGTCAATGGCTGAGGTGAAC 1520
QY 1201 AAGACCTTCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGCATGTGGAGGAACCTCAGC 1260
DB 1521 AAGACCTTCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGCATGTGGAGGAACCTCAGC 1580
QY 1261 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGAOCTTGTCCGGATGCTGTTG 1320
DB 1581 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGAOCTTGTCCGGATGCTGTTG 1640
QY 1321 GACAGAGGACAAATGACCACCTTTTGGGACAGCACTTGGATGGCTTAGATGGACAGCC 1380
DB 1641 GACAGAGGACAAATGACCACCTTTTGGGACAGCACTTGGATGGCTTAGATGGACAGCC 1700
QY 1381 CAAGACATCGTGGCTTTTGGCCAAAGCCACAGAGGATGTCAGTCCAGTAAATGTTCT 1440
DB 1701 CAAGACATCGTGGCTTTTGGCCAAAGCCACAGAGGATGTCAGTCCAGTAAATGTTCT 1760
QY 1441 GTGTACACCTGGAGAGAGCTTTCAAGGACATTAACGAGCAATCCGGACCAATCTCGC 1500
DB 1761 GTGTACACCTGGAGAGAGCTTTCAAGGACATTAACGAGCAATCCGGACCAATCTCGC 1820
QY 1501 TTCAATGAGTGTGTCACCTGAAACAGCTAGAACCCTAGCAACAGAAAGTCTGGCTCATC 1560
DB 1821 TTCAATGAGTGTGTCACCTGAAACAGCTAGAACCCTAGCAACAGAAAGTCTGGCTCATC 1880
QY 1561 AACAACTCCATGAGGAGCTGTGATGAGAGAAATCTTGGGCTGGTATGTTGTTCACTGGA 1620
DB 1881 AACAACTCCATGAGGAGCTGTGATGAGAGAAATCTTGGGCTGGTATGTTGTTCACTGGA 1940
QY 1621 ATTACTCCAGGACATTTAGCTGCCCATCATGTCAAGTACAAGATCCGAAATGGACAT 1680
DB 1941 ATTACTCCAGGACATTTAGCTGCCCATCATGTCAAGTACAAGATCCGAAATGGACAT 2000
QY 1681 GACAATGTGAGGAGGACAAATAAATCAAGATGGGTACTGGACCTGTGCTCTGAGCT 1740
DB 2001 GACAATGTGAGGAGGACAAATAAATCAAGATGGGTACTGGACCTGTGCTCTGAGCT 2060
QY 1741 GACCCCTTTGAGGACATCGCGTAGCTGTGGGGGCTTCGCCCTACTTGCAGGATGGTG 1800
DB 2061 GACCCCTTTGAGGACATCGCGTAGCTGTGGGGGCTTCGCCCTACTTGCAGGATGGTG 2120
QY 1801 GAGCAGCAATCATCAGGGTGTGACGGGACCCGAGAGAAACTGGTGTCTATATGCAA 1860
DB 2121 GAGCAGCAATCATCAGGGTGTGACGGGACCCGAGAGAAACTGGTGTCTATATGCAA 2180
QY 1861 CAGATGCCCTATCCCTGTTAGTTGATGACATCTTTTGGGGGTGATGACCCGCTCAATG 1920
DB 2181 CAGATGCCCTATCCCTGTTAGTTGATGACATCTTTTGGGGGTGATGACCCGCTCAATG 2240
QY 1921 CCCCTCTTCATGACCTGGCTGGATTTACTACGTGGCTGTGATCATCAAGGGCATCGTG 1980

DB 2241 CCCCTCTTCATGAGCTGGCTGGATTTACTACGTGGCTGTGATCATCAAGGGCATCGTG 2300
QY 1981 TATGAGAAAGGAGGACCGCTGAAAGAGACCATGGGATCATGGCCCTGGCAACAGACATA 2040
DB 2301 TATGAGAAAGGAGGACCGCTGAAAGAGACCATGGGATCATGGCCCTGGCAACAGACATC 2360
QY 2041 CTCGTGTTTACCTGGTTCATTAAGTAGAGCTCAATCTCTCTTCTTGTGACGGCTGGCTGCTA 2100
DB 2361 CTCGTGTTTACCTGGTTCATTAAGTAGAGCTCAATCTCTCTTCTTGTGACGGCTGGCTGCTA 2420
QY 2101 GTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTATCCAGCCTGCTGTTGTC 2160
DB 2421 GTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTATCCAGCCTGCTGTTGTC 2480
QY 2161 TTCTGTCCGTGTTGCTGTGGTGACAAATCCTGAGTGTCTTCTGATTAGACACTCTTC 2220
DB 2481 TTCTGTCCGTGTTGCTGTGGTGACAAATCCTGAGTGTCTTCTGATTAGACACTCTTC 2540
QY 2221 TCCAGAGCAACCTGGCAGCAGCCTGTGGGGCATCATCTACTTTCACACTGTACTGCTGCC 2280
DB 2541 TCCAGAGCAACCTGGCAGCAGCCTGTGGGGCATCATCTACTTTCACACTGTACTGCTGCC 2600
QY 2281 TACGTCTCTGTGTGGCATGGCAGACTACGTGGGCTTTCACACTCAAGATCTTGGCTAGC 2340
DB 2601 TACGTCTCTGTGTGGCATGGCAGACTACGTGGGCTTTCACACTCAAGATCTTGGCTAGC 2660
QY 2341 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTGGCCCTTTTGGAGGAGCAG 2400
DB 2661 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTGGCCCTTTTGGAGGAGCAG 2720
QY 2401 GGCATTGGAGTGCAGTGGGACAACTGTTTGGAGTCTCTGTGGAGAAAGATGGCTTCAAT 2460
DB 2721 GGCATTGGAGTGCAGTGGGACAACTGTTTGGAGTCTCTGTGGAGAAAGATGGCTTCAAT 2780
QY 2461 CTCACACTTCCATCTCCATGATGCTGTTGACACTTCTCTATGSGGTGATGACCTGG 2520
DB 2781 CTCACACTTCCATCTCCATGATGCTGTTGACACTTCTCTATGSGGTGATGACCTGG 2840
QY 2521 TACATTGAGCTGTCTTCCAGGCCAGTACGGAATTCACAGCCCTGTGTTTCTCTGTC 2580
DB 2841 TACATTGAGCTGTCTTCCAGGCCAGTACGGAATTCACAGCCCTGTGTTTCTCTGTC 2900
QY 2581 ACCAAGTCTCTACTGTTTGGGAGGAAAGTGTGAGAGAGCCACCTGGTGTCCAAACAG 2640
DB 2901 ACCAAGTCTCTACTGTTTGGGAGGAAAGTGTGAGAGAGCCACCTGGTGTCCAAACAG 2960
QY 2641 AAGAGAAATGTCAAGAAATCTGATGGAGGAGAAACCCACCTTGAAGCTGGCGGTGTC 2700
DB 2961 AAGAGAAATGTCAAGAAATCTGATGGAGGAGAAACCCACCTTGAAGCTGGCGGTGTC 3020
QY 2701 ATTCAAGACCTGGTAAAAGTCTACCGAGAGGGATGAAGTGGCTGCTCGATGGCTGGCA 2760
DB 3021 ATTCAAGACCTGGTAAAAGTCTACCGAGATGGGATGAAGTGGCTGCTCGATGGCTGGCA 3080
QY 2761 CTGAATTTTATGAGGCCAGATCACCTCTTCTGGGCCAACAAATGGAGCGGGAAGAGC 2820
DB 3081 CTGAATTTTATGAGGCCAGATCACCTCTTCTGGGCCAACAAATGGAGCGGGAAGAGC 3140
QY 2821 ACCACCATGTCAATCTGACCGGGTTTCCCCCCCCACCTCGGGCACCCCTACATCTCTG 2880
DB 3141 ACCACCATGTCAATCTGACCGGGTTTCCCCCCCCACCTCGGGCACCCCTACATCTCTG 3200
QY 2881 GGAAGACATTCGCTCTGAGTAGACCACTCCGGCAGAACCTGGGGGTCTGCTCCCGAG 2940
DB 3201 GGAAGACATTCGCTCTGAGTAGACCACTCCGGCAGAACCTGGGGGTCTGCTCCCGAG 3260
QY 2941 CATAAGCTGTGTTGACATGCTGACTGTGGAAGAACACATCTGTTTCTATGCCCGCTTG 3000
DB 3261 CATAAGCTGTGTTGACATGCTGACTGTGGAAGAACACATCTGTTTCTATGCCCGCTTG 3320
QY 3001 AAAGGGCTCTCTGAGAGACCTGTAAGGGCGGAGATGGAGCAGATGGCCCTGATGTTGGT 3060

QY	4141	CCCTGGATGTACAACGAACAGATACACATTTGTGACGAATGATGCTCCTGAGGACACGGGA	4200
Db	4461	CCCTGGATGTACAAGGAACAGATACACATTTGTGACGAATGATGCTCCTGAGGACACGGGA	4520
QY	4201	ACCTTGGAACTCTTAAACGCCCTCACCAAAGACCCCTGGCTTGGGACCCGCTGTATGAA	4260
Db	4521	ACCTTGGAACTCTTAAAGCCCTCACCAAAGACCCCTGGCTTGGGACCCGCTGTATGAA	4580
QY	4261	GGAAACCCCAATCCAGACACGCCCTGCAGGACGAGGGAGAAAGTGGACCACTGCCCA	4320
Db	4581	GGAAACCCCAATCCAGACACGCCCTGCAGGACGAGGGAGAAAGTGGACCACTGCCCA	4640
QY	4321	GTTCGCCAGACCATCATGAGCCTCTCCAGAAATGGAACTGGACAATGGACAACCTTCA	4380
Db	4641	GTTCGCCAGACCATCATGAGCCTCTCCAGAAATGGAACTGGACAATGGACAACCTTCA	4700
QY	4381	CCTGCATGCCAGTGTAGCAGGACACAAAATCAAGAAATGCTGCCGTGTGTGCCCAAGG	4440
Db	4701	CCTGCATGCCAGTGTAGCAGGACACAAAATCAAGAAATGCTGCCGTGTGTGCCCAAGG	4760
QY	4441	GCAGGGGGCTGCCCTCCTCCACAAAGAAACAAACACATGCAATATCCTTCAGACCTG	4500
Db	4761	GCAGGGGGCTGCCCTCCTCCACAAAGAAACAAACACATGCAATATCCTTCAGACCTG	4820
QY	4501	ACAGGAAGAAACATTCGSGATTATCTGGTCAAGACGTATGTCCAGCATCATGCCAAAGC	4560
Db	4821	ACAGGAAGAAACATTCGSGATTATCTGGTCAAGACGTATGTCCAGCATCATGCCAAAGC	4880
QY	4561	TTAAGAAACAAGATCTGGGTCAATGATTTAGTATGGCGGCTTTTCCCTGGGTGTCAGT	4620
Db	4881	TTAAGAAACAAGATCTGGGTCAATGATTTAGTATGGCGGCTTTTCCCTGGGTGTCAGT	4940
QY	4621	TAATCTCAAGCACTTCCTCCGAGTCAAGAGTTATGATGCAATCAACAAATGAAGAA	4680
Db	4941	TAATCTCAAGCACTTCCTCCGAGTCAAGAGTTATGATGCAATCAACAAATGAAGAA	5000
QY	4681	CACCTAAAGCTGGCCAAAGGACATTCCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT	4740
Db	5001	CACCTAAAGCTGGCCAAAGGACATTCCTGCAGATCGATTTCTCAACAGCTTGGGAAGATT	5060
QY	4741	ATGACAGCATGGACACCAGAAATATGTCAAGTGTGGTTCAATAACAAGGCTGGCAT	4800
Db	5061	ATGACAGCATGGACACCAGAAATATGTCAAGTGTGGTTCAATAACAAGGCTGGCAT	5120
QY	4801	GCAATCAGCTCTTCCCTGAAATGTCATCAACATGCCATTCCTCCGGGCCACCTGCAAAAG	4860
Db	5121	GCAATCAGCTCTTCCCTGAAATGTCATCAACATGCCATTCCTCCGGGCCACCTGCAAAAG	5180
QY	4861	GGAGAGAACCCTAGCCATPATGGAATFACCTGTTTCAATCATCCCTGAAATCACCAG	4920
Db	5181	GGAGAGAACCCTAGCCATPATGGAATFACCTGTTTCAATCATCCCTGAAATCACCAG	5240
QY	4921	CAGCAGCTCTCAGAGTGGCTGTATGACCAATCAGTGGATGCTCTGTCCTCATCTGT	4980
Db	5241	CAGCAGCTCTCAGAGTGGCTGTATGACCAATCAGTGGATGCTCTGTCCTCATCTGT	5300
QY	4981	GTCACTTTTGCATGTCTTCGTCCGACCAAGCTTTGCTGATTCCTGATCCAGAGCGG	5040
Db	5301	GTCACTTTTGCATGTCTTCGTCCGACCAAGCTTTGCTGATTCCTGATCCAGAGCGG	5360
QY	5041	GTGAGAAAGCAAAACACCTGCAGTTCATCAGTGGATGAAGCCTGTATCTACTGGCTC	5100
Db	5361	GTGAGAAAGCAAAACACCTGCAGTTCATCAGTGGATGAAGCCTGTATCTACTGGCTC	5420
QY	5101	TCTAATTTTGTCTGGGATATGCAATTAACGTTGTCCCTGCCACATGGTCAATATCATC	5160
Db	5421	TCTAATTTTGTCTGGGATATGCAATTAACGTTGTCCCTGCCACATGGTCAATATCATC	5480
QY	5161	TTCACTGCTCTCCAGCAGAGTCTCTATGTCTCTCCAAATCTGCTGTGCTGTAGCCCTT	5220
Db	5481	TTCACTGCTCTCCAGCAGAGTCTCTATGTCTCTCCAAATCTGCTGTGCTGTAGCCCTT	5540

5221 CTACTTTGCTGATGGTGGTCAATCACACCTCTCATGTACCCAGCCTCTTTTGTTGTC 5280
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5281 AAGATCCCCAGCACACCTATGTGTGTCTACCCAGCGTGAACCTCTTTCATTGGCAATTAAT 5340
5601 AAGATCCCCAGCACACCTATGTGTGTCTACCCAGCGTGAACCTCTTTCATTGGCAATTAAT 5660
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5721 GATATCCTGAAGTCCGTGTCTTGTGATCTTCCACATATTTTGGCTGGGACGAGGCTCATC 5780
5461 GACATGGTGAATAACACAGCAATGGCTGATGCCCTGGGAAGGTTTGGGAGAAATGCTTT 5520
5781 GACATGGTGAATAACACAGCAATGGCTGATGCCCTGGGAAGGTTTGGGAGAAATGCTTT 5840
5521 GTGTCAACCATTTCTTGGGACTTGGTGGGACGAAACCTCTTGGCCATGGCCCTGGAAGGG 5580
5841 GTGTCAACCATTTCTTGGGACTTGGTGGGACGAAACCTCTTGGCCATGGCCCTGGAAGGG 5900
5581 GTGGTCTTCTTCCCTAATTAATCTGTCTGATCCAGTACAGATTTCTTATCAGGCCAGCACT 5640
5901 GTGGTCTTCTTCCCTAATTAATCTGTCTGATCCAGTACAGATTTCTTATCAGGCCAGCACT 5960
5641 GTAATGCAAGGATCTCTCTGAATGATGAAGTGAAGTGTGAGCGGGAAGACAG 5700
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5761 TATAGAAGGAGCGGAGCCTGCTGTGTGACAGATTTGGTGGCAATCTCTCTGCTGTGAG 5820
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5821 TGCTTTGGGCTCTGGGAGTAAATGGGCTGGAATATCAACTTCAAGATGTTAAACA 5880
6141 TGCTTTGGGCTCTGGGAGTAAATGGGCTGGAATATCAACTTCAAGATGTTAAACA 6200
5881 GGAGATACCACTGTATACAGAGAGATGCTTCTTCTTAAACAAATAGTATCTTATCAAAC 5940
6201 GGAGATACCACTGTATACAGAGAGATGCTTCTTCTTAAACAAATAGTATCTTATCAAAC 6260
5941 ATCCATCAAGTACATCAGACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6000
6261 ATCCATCAAGTACATCAGACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6320
6001 TTGACTGGGAGAGAACACGTGGAGTCTTTGGCCCTTTTGAGAGAGTCCACAGAGAAGAA 6060
6321 TTGACTGGGAGAGAACACGTGGAGTCTTTGGCCCTTTTGAGAGAGTCCACAGAGAAGAA 6380
6061 GTTGGCAGAGTTGCTGAGTGGCATTGCGAACTGGCCCTCGTGAAGTATGGAGAAAAA 6120
6381 GTTGGCAGAGTTGCTGAGTGGCATTGCGAACTGGCCCTCGTGAAGTATGGAGAAAAA 6440
6121 TATGCTGTTACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
6441 TATGCTGTTACTATAGTGGAGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6500
6181 GCGGGGCTCTCTGTTGTTTCTGGATGAACCCACACAGCATGGATCCCAAGCCCGG 6240
6501 GCGGGGCTCTCTGTTGTTTCTGGATGAACCCACACAGCATGGATCCCAAGCCCGG 6560
6241 CGGTTCTTGTGAATTTGTCCTTAAGTGTGTTCAAGGAGGGAGATCAGTAGTCTTACA 6300
6561 CGGTTCTTGTGAATTTGTCCTTAAGTGTGTTCAAGGAGGGAGATCAGTAGTCTTACA 6620
6301 TCTCATAGTATGGAAGATGGAAGTCTTTGCACTAGGATGGCAATCGTCAATCGA 6360

6621 TCTCATAGTATGGAAGATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA 6680
6361 AGGTTCCAGTCCCTTGGCAGTGTCCAGCATCTAAAATAGTTTGGAGATGGTTATACA 6420
6681 AGGTTCCAGTCCCTTGGCAGTGTCCAGCATCTAAAATAGTTTGGAGATGGTTATACA 6740
6421 ATAGTTGTACGAATAGCAGGCTCCAAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6480
6741 ATAGTTGTACGAATAGCAGGCTCCAAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6800
6481 CTTCGATTTCTTGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACATAATACAGCTT 6540
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6541 CCATCTTTCATTTCTCTGCTGCCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA 6600
6861 CCATCTTTCATTTCTCTGCTGCCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA 6920
6601 CTCCACATAGAACTACTCTGTTTCTCAGACACACTTTGACCAAGTATTTGTGAACHTT 6660
6921 CTCCACATAGAACTACTCTGTTTCTCAGACACACTTTGACCAAGTATTTGTGAACHTT 6980
6661 GCCAAGGACCAAGTGTGATGACCACTTAAAGACCTCTCATACACAAAACCCAGACA 6720
6981 GCCAAGGACCAAGTGTGATGACCACTTAAAGACCTCTCATACACAAAACCCAGACA 7040
6721 GTAGTGGAGCTTGGAGTCTTCACATCTTTTCTACAGATGAGAAAGTGAAGAAGCTAT 6780
7041 GTAGTGGAGCTTGGAGTCTTCACATCTTTTCTACAGATGAGAAAGTGAAGAAGCTAT 7100
6781 GTAT 6784
7101 GTAT 7104

RESULT 11
AAS06120
ID AAS06120 standard; cDNA; 9741 BP.
XX
AC AAS06120;
XX
DT 12-SEP-2001 (first entry)
XX
DE Human ABC1 DNA sequence #1.
XX
KW Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
cardiovascular; neurological; Tangier disease; LCAT deficiency;
lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 185..6967
FT /tag= a
FT /product= "Human ABC1 protein"
XX
WO200130848-A2.
PN
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-BP10886.
XX
PR 26-OCT-1999; 99EP-0402668.
PR 01-MAR-2000; 2000US-0186260.
XX
PA (AVET) AVENTIS PHARMA SA.
XX
PI Deneffe P, Rosier-Montus M, Arnould-Requigne I, Prades C, Naudin L;
Lemoline C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
Dean M;
XX
WPI; 2001-316327/33.

DR P-PSDB; AAU02176.

XX New human ABC1 nucleic acids and polypeptides for treating
PT atherosclerosis, malaria and diabetes -
XX

PS Claim 1; Page 204-208; 368pp; English.

XX The sequence represents the coding sequence #1 of human ABC1. The
CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
CC and polypeptides and vectors are useful for the prevention of
CC atherosclerosis, in a subject affected by a dysfunction in the reverse
CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
CC useful for screening for an active ingredient for the prevention or
CC treatment of a disease resulting from dysfunction in the reverse
CC transport of cholesterol. The nucleic acids and polypeptides are also
CC useful for treating and preventing cardiovascular and neurological
CC pathologies, and other diseases e.g. Tangier disease, lecithin-
XX cholesterol (LCAT) deficiency, malaria and diabetes.

SQ Sequence 9741 BP; 2650 A; 2180 C; 2290 G; 2620 T; 1 other;

Query Match 99.7%; Score 6764.8; DB 22; Length 9741;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy	1	ATGGCTTGTGGCTCAGCTGAGTTCTGCTGTGGAGAACCTCCTCTCAGAGAAGA	60
Db	185	ATGGCTTGTGGCTCAGCTGAGTTCTGCTGTGGAGAACCTCCTCTCAGAGAAGA	244
Qy	61	CAACATGTCAGCTGTTACTGGAAGTGGCTGCTCTATTTATCTCTCTGATC	120
Db	245	CAACATGTCAGCTGTTACTGGAAGTGGCTGCTCTATTTATCTCTCTGATC	304
Qy	121	TCTGTTCGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTCCAAATAAGCC	180
Db	305	TCTGTTCGGCTGAGCTACCCACCTATGAACACATGAATGCCATTTCCAAATAAGCC	364
Qy	181	ATGGCTCTGAGAACACATTCCTTGGTTTCTGAGGATATCTGTAATGCCAACACCC	240
Db	365	ATGGCTCTGAGAACACATTCCTTGGTTTCTGAGGATATCTGTAATGCCAACACCC	424
Qy	241	TGTTTCCGTTACCGACTCTGCGGAGGCTCCCGGAGTTGTTGGAACTTTTAACTTCC	300
Db	425	TGTTTCCGTTACCGACTCTGCGGAGGCTCCCGGAGTTGTTGGAACTTTTAACTTCC	484
Qy	301	ATTGTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCAGAAAGACAC	360
Db	485	ATTGTGGCTGCCCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCAGAAAGACAC	544
Qy	361	AGCATGAAGGACATGCGGAAGTTCTGAGAACATTAACAGAGATCAAGAAATCCAGCTCA	420
Db	545	AGCATGAAGGACATGCGGAAGTTCTGAGAACATTAACAGAGATCAAGAAATCCAGCTCA	604
Qy	421	AACCTTGAAGCTTCAAGATTTCCCTGGTGGACAATGAACCTTCTCTGGTTCCCTATATAC	480
Db	605	AACCTTGAAGCTTCAAGATTTCCCTGGTGGACAATGAACCTTCTCTGGTTCCCTATATAC	664
Qy	481	AACCTTCTCTCCCAAGTCTACTGTGGACAAGATGCTGAGGCTGATGTCTATCTCCAC	540
Db	665	AACCTTCTCTCCCAAGTCTACTGTGGACAAGATGCTGAGGCTGATGTCTATCTCCAC	724
Qy	541	AAGTATTTTGGAGGCTACCACTTACATTTGACAGTCTGTGCAATGGATCAAAATCA	600
Db	725	AAGTATTTTGGAGGCTACCACTTACATTTGACAGTCTGTGCAATGGATCAAAATCA	784
Qy	601	GAAGAGATGATTAACCTTGTGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAAGAGG	660
Db	785	GAAGAGATGATTAACCTTGTGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAAGAGG	844
Qy	661	AACTGGCTGAGCAGAGGAGTACTTCTGTTCCAAATGGACATCTGAGGCCAATCTCTG	720
Db	845	AACTGGCTGAGCAGAGGAGTACTTCTGTTCCAAATGGACATCTGAGGCCAATCTCTG	904

Qy	721	AGAACACTAACTCTACATCTCCCTTCCGAGCAAGAGAGCTGGCTGAGCCACAAAACA	780
Db	905	AGAACACTAACTCTACATCTCCCTTCCGAGCAAGAGAGCTGGCTGAGCCACAAAACA	964
Qy	781	TTGCTGATAGTCTTGGGACTCTGCCCCAGGAGCTGTTCAGCATGAGAGAGCTGGAGTAC	840
Db	965	TTGCTGATAGTCTTGGGACTCTGCCCCAGGAGCTGTTCAGCATGAGAGAGCTGGAGTAC	1024
Qy	841	ATGGACAGAGAGGTGATGTTCTGACCAATGTGAACAGTCCAGCTCTCCACCCAAATC	900
Db	1025	ATGGACAGAGAGGTGATGTTCTGACCAATGTGAACAGTCCAGCTCTCCACCCAAATC	1084
Qy	901	TACCAGGCTGTCTCTGCTGTTCTGCTGGGCATCCCGAGGAGGGGGCTGAAGATCAAG	960
Db	1085	TACCAGGCTGTCTCTGCTGTTCTGCTGGGCATCCCGAGGAGGGGGCTGAAGATCAAG	1144
Qy	961	TCTCTCAACTGATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1020
Db	1145	TCTCTCAACTGATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1204
Qy	1021	CAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG	1080
Db	1205	GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG	1264
Qy	1081	AATTGGAGTCTAGTCTCTTCTCCGCAATATCTGGAAGCTCTGAAGCGCTGCTCGTT	1140
Db	1265	AATTGGAGTCTAGTCTCTTCTCCGCAATATCTGGAAGCTCTGAAGCGCTGCTCGTT	1324
Qy	1141	GGGAGATCTCTGTATACACCTGACACTCCAGCCACCAAGGCAAGTGGTGAAGTGAAC	1200
Db	1325	GGGAGATCTCTGTATACACCTGACACTCCAGCCACCAAGGCAAGTGGTGAAGTGAAC	1384
Qy	1201	AAGACCTTCCAGGAACCTGGCTGTTCCATGATCTGGAAGGCAATGGGAGGAACTCAGC	1260
Db	1385	AAGACCTTCCAGGAACCTGGCTGTTCCATGATCTGGAAGGCAATGGGAGGAACTCAGC	1444
Qy	1261	CCCAAGATCTGAGACTTTCATGGAGAACAGCAAGAAATGACCTTGTCCGGATGCTGTTG	1320
Db	1445	CCCAAGATCTGAGACTTTCATGGAGAACAGCAAGAAATGACCTTGTCCGGATGCTGTTG	1504
Qy	1321	GACAGCAGGACATGACCACTTTTGGGACACAGCATTTGGATGGCTTAGATGGACAGCC	1380
Db	1505	GACAGCAGGACATGACCACTTTTGGGACACAGCATTTGGATGGCTTAGATGGACAGCC	1564
Qy	1381	CAAGACATCTGGGCTTTTGGCCCAAGCACCAGAGAGTGTCCAGTCCAGTAAATGTTCT	1440
Db	1565	CAAGACATCTGGGCTTTTGGCCCAAGCACCAGAGAGTGTCCAGTCCAGTAAATGTTCT	1624
Qy	1441	GTGTACACCTGGAGAGAGCTTTCAACGAGACTTAACAGGCAATCCGGACCATATCTCCG	1500
Db	1625	GTGTACACCTGGAGAGAGCTTTCAACGAGACTTAACAGGCAATCCGGACCATATCTCCG	1684
Qy	1501	TTCATGGAGTGTCTCAACCTGAACAACTAGAACCCATAGAACAGAGTCTGGCTCATC	1560
Db	1685	TTCATGGAGTGTCTCAACCTGAACAACTAGAACCCATAGAACAGAGTCTGGCTCATC	1744
Qy	1561	AACAAGTCCATGGAGTGTCTGGATGAGAGAGTCTGGGCTGGTATGTTGTTCACTGA	1620
Db	1745	AACAAGTCCATGGAGTGTCTGGATGAGAGAGTCTGGGCTGGTATGTTGTTCACTGA	1804
Qy	1621	ATTACTCCAGCAGCATTTGAGTCTCCCATCATGTCAAGTACAAAGATCCGAATGGACATT	1680
Db	1805	ATTACTCCAGCAGCATTTGAGTCTCCCATCATGTCAAGTACAAAGATCCGAATGGACATT	1864
Qy	1681	GACAAATGTGGAGAGCAAAATAAATCAAGATGGGTACTGGACCCCTGGTCTCCAGCT	1740
Db	1865	GACAAATGTGGAGAGCAAAATAAATCAAGATGGGTACTGGACCCCTGGTCTCCAGCT	1924
Qy	1741	GACCCCTTTGAGGACATGCGGTAGCTCTGGGGGGGCTTCCCTTACTTGCAGGATGTGGTG	1800
Db	1925	GACCCCTTTGAGGACATGCGGTAGCTCTGGGGGGGCTTCCCTTACTTGCAGGATGTGGTG	1984
Qy	1801	GAGCAGGCAATCATCAGGTGCTGACGGGACCGAGAGAAACTGGTGTCTATATGCAA	1860

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Db 1985 GAGCAGCAATCATCAGGTGCTGACGGGCACGAGAGAAACTGGTGTCTATATGCAA 2044
QY 1861 CAGATCCCTATCCCTGTTACGTTGATGACATCTTCTCGGGGTGATGAGCCGGTCAATG 1920
Db 2045 CAGATCCCTATCCCTGTTACGTTGATGACATCTTCTCGGGGTGATGAGCCGGTCAATG 2104
QY 1921 CCCTCTTATGACGCTGGCCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1980
Db 2105 CCCTCTTATGACGCTGGCCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 2164
QY 1981 TATGAGAAGGAGCAGCGGTGAAAGAGACCATCGGATCATGGGCTGGACAAACAGCATA 2040
Db 2165 TATGAGAAGGAGCAGCGGTGAAAGAGACCATCGGATCATGGGCTGGACAAACAGCATA 2224
QY 2041 CTCGTGTTAGCTGGTTCATTAGTAGCCCTATTCTCTTCTTGTAGCGCTGGCTGTCTA 2100
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QY 2101 GTGGTCATCCTGAAGTTAGAAACCTGCTGCCCTACAGTGAATCCAGCGCTGGTGTGTC 2160
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QY 2161 TTCTCTGCGTGTTCCTGTGTGTGACAACTCTGCAGTGTCTCTGATTAGCACACTCTTC 2220
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QY 2221 TCAGAGCCAACTGGCAGCAGCGCTGTGGGGGCATCATCTACTTACCGCTGTACCTGCC 2280
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QY 2521 TACATTGAGGCTGTCTTCCAGGCCAGTACGGAAATCCAGGCCCTGGTATTTTCCCTTC 2580
Db 2705 TACATTGAGGCTGTCTTCCAGGCCAGTACGGAAATCCAGGCCCTGGTATTTTCCCTTC 2764
QY 2581 ACCAAGTCTACTGGTTTGGCGAGGAAAGTGTGAGAGAGCCACCTGGTTCCCAACCGAG 2640
Db 2765 ACCAAGTCTACTGGTTTGGCGAGGAAAGTGTGAGAGAGCCACCTGGTTCCCAACCGAG 2824
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Db 2825 AAGAGAATGTCAGAAATCTCATGGAGGAGAACCCACCCACTTGAAGCTGGGCGTGTCC 2884
QY 2701 ATTCAGAACCTGTTAAAGTCTACCGAGATGGGATGGAAGTGGCTGTGATGGCCCTGGCA 2760
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Db 3065 GGAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAAACCTCGGGGTCTGTCCCCAG 3124
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QY 3061 TTGCCATCAAGCAAGCTGAAAAGCAAAACAGCCAGCTGTGAGTGGGAATGCAGAGAAAG 3120
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QY 3301 ATTGCCATCATCTCCCATGGGAGCTGTGCTGTGGGCTCTCTCCCTGTTTCTGAAGAAC 3360
Db 3485 ATTGCCATCATCTCCCATGGGAGCTGTGCTGTGGGCTCTCTCCCTGTTTCTGAAGAAC 3544
QY 3361 CAGCTGGGAACAGCTACTACTGACCTTGCTCAAGAAAGATGTGGAATCTCCCTCAGT 3420
Db 3545 CAGCTGGGAACAGCTACTACTGACCTTGCTCAAGAAAGATGTGGAATCTCCCTCAGT 3604
QY 3421 TCCTGCAGAAACAGTAGTAGCACTGTGTACACCTGATAACCTGATAAGAGGAGCAGTGTTCAG 3480
Db 3605 TCCTGCAGAAACAGTAGTAGCACTGTGTACACCTGATAAGAGGAGCAGTGTTCAG 3664
QY 3481 ACAGTTCTGATGCTGGCTGGGAGCCACCATGAGATGACACCTGACCATCATGCTC 3540
Db 3665 ACAGTTCTGATGCTGGCTGGGAGCCACCATGAGATGACACCTGACCATCATGCTC 3724
QY 3541 TCTGTATCTCCAACTCATCAGGAAGATGTGTCTGAAGCCCGCTGTGTGAAGACATA 3600
Db 3725 TCTGTATCTCCAACTCATCAGGAAGATGTGTCTGAAGCCCGCTGTGTGAAGACATA 3784
QY 3601 GGGCATGAGCTGACCTATGCTGCCATGAAGTGTCTAAGAGGAGGAGCCTTTGTGAA 3660
Db 3785 GGGCATGAGCTGACCTATGCTGCCATGAAGTGTCTAAGAGGAGGAGCCTTTGTGAA 3844
QY 3661 CTCTTTCATGAGATTGATGACCGCTCTCAGACCTGGGCATTTCTAGTATGSCATCTCA 3720
Db 3845 CTCTTTCATGAGATTGATGACCGCTCTCAGACCTGGGCATTTCTAGTATGSCATCTCA 3904
QY 3721 GAGCAGACCTTGGAGAAATATTCTCAAGGTGGCCGAGAGAGTGGGTGGATGCTGAG 3780
Db 3905 GAGCAGACCTTGGAGAAATATTCTCAAGGTGGCCGAGAGAGTGGGTGGATGCTGAG 3964
QY 3781 ACCTCAGATGGTACCTTCCAGCAAGACAAACAGCGGGCCCTTGGGGACAGCAGACG 3840
Db 3965 ACCTCAGATGGTACCTTCCAGCAAGACAAACAGCGGGCCCTTGGGGACAGCAGACG 4024
QY 3841 TGTCTTCGCGCGTTCACTCAAGATGATGCTGTGATPCCAAATGATTCTGACATAGACCA 3900
Db 4025 TGTCTTCGCGCGTTCACTCAAGATGATGCTGTGATPCCAAATGATTCTGACATAGACCA 4084
QY 3901 GAATCCAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAAAGGTCCTTACCAGGTGAAA 3960
Db 4085 GAATCCAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAAAGGTCCTTACCAGGTGAAA 4144
QY 3961 GCTGTGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTTAATTGC 4020
Db 4145 GCTGTGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTTAATTGC 4204

Qy	5101	TCTAATTTTGCTGGGATATGTGCAATTAAGTTGTCCCTGCCACACTGGTCATTATCAATC	5160
Db	5285	TCTAATTTTGCTGGGATATGTGCAATTAAGTTGTCCCTGCCACACTGGTCATTATCAATC	5344
Qy	5161	TTCAATCGCTTCCAGCAGAAGTCCTATATGTGCTCTCCACCAATCTGCCTGTGCTAGCCCTT	5220
Db	5345	TTCAATCGCTTCCAGCAGAAGTCCTATATGTGCTCTCCACCAATCTGCCTGTGCTAGCCCTT	5404
Qy	5221	CTACTTTTGTGTATGGTGGTCAATCACACACTCTCATGTACCACGCTCCTTTGTGTTC	5280
Db	5405	CTACTTTTGTGTATGGTGGTCAATCACACACTCTCATGTACCACGCTCCTTTGTGTTC	5464
Qy	5281	AAGATCCCGACGACACCCATATGTTGGTCTCACCAGGTGAACCTCTTCAATGGCATTAAT	5340
Db	5465	AAGATCCCGACGACACCCATATGTTGGTCTCACCAGGTGAACCTCTTCAATGGCATTAAT	5524
Qy	5341	GGCAGCGTGGCCACCTTTGTGTGTGAGCTGTTCACCGACAATAAGCTGAATAATATCAAT	5400
Db	5525	GGCAGCGTGGCCACCTTTGTGTGTGAGCTGTTCACCGACAATAAGCTGAATAATATCAAT	5584
Qy	5401	GATATCCTGAAGTCCGTGTTCTTGATCTTCCACATATTTTGGCTGGGAGAGGCTCATC	5460
Db	5585	GATATCCTGAAGTCCGTGTTCTTGATCTTCCACATATTTTGGCTGGGAGAGGCTCATC	5644
Qy	5461	GACATGTTGAAAAACACGAGCAATGGCTGATGCCCTGGAAGGTTTGGGAGAAATCGCTTT	5520
Db	5645	GACATGTTGAAAAACACGAGCAATGGCTGATGCCCTGGAAGGTTTGGGAGAAATCGCTTT	5704
Qy	5521	GTGTACCACTATCTTGGGACTTGTGGGAGAAACCTCTTGGCATGGCCGTGGAAGGG	5580
Db	5705	GTGTACCACTATCTTGGGACTTGTGGGAGAAACCTCTTGGCATGGCCGTGGAAGGG	5764
Qy	5581	GTGGTGTCTTCTCATTAATCTGTCTGATCCAGTACAGATTTCTCATCAGGCCAGACCT	5640
Db	5765	GTGGTGTCTTCTCATTAATCTGTCTGATCCAGTACAGATTTCTCATCAGGCCAGACCT	5824
Qy	5641	GTAATGCAAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGCGGGGAAGACAG	5700
Db	5825	GTAATGCAAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGCGGGGAAGACAG	5884
Qy	5701	AGAATCTTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGAGGTTGACCAAGATA	5760
Db	5885	AGAATCTTGATGGTGGAGCCAGATGACATCTTAGAAATCAAGAGGTTGACCAAGATA	5944
Qy	5761	TATAGAAGGAAGCGAAGCGCTGCTGTGTACAGAGATTTCGGTGGGCATTCCTCCTGGTGA	5820
Db	5945	TATAGAAGGAAGCGAAGCGCTGCTGTGTACAGAGATTTCGGTGGGCATTCCTCCTGGTGA	6004
Qy	5821	TGCTTTGGCTCCTGGAGTTTAATGGGCGTGAAAAATCATCACTTTCAAGATGTTAACA	5880
Db	6005	TGCTTTGGCTCCTGGAGTTTAATGGGCGTGAAAAATCATCACTTTCAAGATGTTAACA	6064
Qy	5881	GGAGATACCACTGTTACAGAGAGATGCTTTCCTTAACAAAAATAGTATCTTATCAAC	5940
Db	6065	GGAGATACCACTGTTACAGAGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAC	6124
Qy	5941	ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGATGCAATCACAGAGCTG	6000
Db	6125	ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGATGCAATCACAGAGCTG	6184
Qy	6001	TTCACTGGGAGAGAACACGTGGAGTTCTTTGGCCCTTTTGAGAGAGTCCAGAGAGAA	6060
Db	6185	TTCACTGGGAGAGAACACGTGGAGTTCTTTGGCCCTTTTGAGAGAGTCCAGAGAGAA	6244
Qy	6061	GTTGCAAGGTTGGTAGTGGCGATTCCGAACCTGGCCCTCGTGAAGTATGGAGAAAA	6120
Db	6245	GTTGCAAGGTTGGTAGTGGCGATTCCGAACCTGGCCCTCGTGAAGTATGGAGAAAA	6304
Qy	6121	TATGCTTGGTAACATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTGATC	6180
Db	6305	TATGCTTGGTAACATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTGATC	6364
Qy	6181	GGCGGCGCTCCTGTGGTGTCTTCGTATGAACCCACACAGCATGGATCCCAAGACCGCG	6240

QY	661	AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAAATGGACATCCTGAGCCCAATCCTG	720
Db	845	AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAAATGGACATCCTGAGCCCAATCCTG	904
QY	721	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGAGCTGCCTGAAGCCACAAAACA	780
Db	905	AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGAGCTGCCTGAAGCCACAAAACA	964
QY	781	TGTGTCGATAGCTCTGGGACATCTGGCCGAGGAGCTGTTCCAGCATGAGAAGCTGGAGTGAC	840
Db	965	TGTGTCGATAGCTCTGGGACATCTGGCCGAGGAGCTGTTCCAGCATGAGAAGCTGGAGTGAC	1024
QY	841	ATGGCAGAGGAGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	900
Db	1025	ATGGCAGAGGAGTGATGTTTCTTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	1084
QY	901	TACCAGGCTGTGCTCGTATTGTCTCGGGGCAATCCGAGGAGGGGGGCTGAAGATCAAG	960
Db	1085	TACCAGGCTGTGCTCGTATTGTCTCGGGGCAATCCGAGGAGGGGGGCTGAAGATCAAG	1144
QY	961	TCTCTCAACTGGTATGAGGACAACTACAAGGCCCTTTTGAGGAGCAATGGCACCTGAG	1020
Db	1145	TCTCTCAACTGGTATGAGGACAACTACAAGGCCCTTTTGAGGAGCAATGGCACCTGAG	1204
QY	1021	GAAATGCTGAAGACCTCTATGACAACTCTACAATCCTTACTGCAATGATTTGATGAAG	1080
Db	1205	GAAATGCTGAAGACCTCTATGACAACTCTACAATCCTTACTGCAATGATTTGATGAAG	1264
QY	1081	AATTTGGAGTCTAGTCTCTCTTTCCGCCATTATCTGGAAGCTCTGAAGCCGCTGCTGTT	1140
Db	1265	AATTTGGAGTCTAGTCTCTCTTTCCGCCATTATCTGGAAGCTCTGAAGCCGCTGCTGTT	1324
QY	1141	GGGAAGATCCTGTATACACTGACACTCCAGCCCAAGGCAAGGTCATGGCTGAGGTGAAC	1200
Db	1325	GGGAAGATCCTGTATACACTGACACTCCAGCCCAAGGCAAGGTCATGGCTGAGGTGAAC	1384
QY	1201	AAGACCTTCCAGAACTGGCTGTGTTTCCATGATCTGGAAGCAGTGGGAGGAACTCAGC	1260
Db	1385	AAGACCTTCCAGAACTGGCTGTGTTTCCATGATCTGGAAGCAGTGGGAGGAACTCAGC	1444
QY	1261	CCCAGATCTGGACCTTCATGAGAGACACCCAAAGAAATGAGACCTTGTCCGGATGCTGTTG	1320
Db	1445	CCCAGATCTGGACCTTCATGAGAGACACCCAAAGAAATGAGACCTTGTCCGGATGCTGTTG	1504
QY	1321	GACAGCAGGACAAATCACCACATTTTGGGAACAGCAGTTGGATGGCTTAGATTTGACAGCC	1380
Db	1505	GACAGCAGGACAAATCACCACATTTTGGGAACAGCAGTTGGATGGCTTAGATTTGACAGCC	1564
QY	1381	CAGACATCGTGGCGTTTTTGGCCAAAGCACCAGAGGATGTCCAGTCCAGTAATGTTCT	1440
Db	1565	CAGACATCGTGGCGTTTTTGGCCAAAGCACCAGAGGATGTCCAGTCCAGTAATGTTCT	1624
QY	1441	GTGTACACCTGGAGAGAGCTTTCAACGAGACTAACACAGCAATCCGGAGCCATATCTCGC	1500
Db	1625	GTGTACACCTGGAGAGAGCTTTCAACGAGACTAACACAGCAATCCGGAGCCATATCTCGC	1684
QY	1501	TTCATGGAGTGTGTCAACCTGAACAGCTAGAACCCATAGCAACAAGTCTGGCTCATC	1560
Db	1685	TTCATGGAGTGTGTCAACCTGAACAGCTAGAACCCATAGCAACAAGTCTGGCTCATC	1744
QY	1561	AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTTCTGGGCTGGTATTGTTCACTGGA	1620
Db	1745	AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTTCTGGGCTGGTATTGTTCACTGGA	1804
QY	1621	ATTACTCCAGGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1680
Db	1805	ATTACTCCAGGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1864
QY	1681	GACAAATGCGGAGAGACAAATAAAATCAAGATGGGTACTGGGACCTGGTCTCGAGCT	1740
Db	1865	GACAAATGCGGAGAGACAAATAAAATCAAGATGGGTACTGGGACCTGGTCTCGAGCT	1924

QY	1741	GACCCCTTTGAGGCACATCGCGGTACGCTCTGGGGGGGCTTCGGCTACTTGCAGGATGTGGT	1800
DB	1925	GACCCCTTTGAGGCACATCGCGGTACGCTCTGGGGGGGCTTCGGCTACTTGCAGGATGTGGT	1984
QY	1801	GAGCAGGCAATCATCAGGTCGTGACGGGCACCGAGAGAAAACHTGGTCTATATGCAA	1860
DB	1985	GAGCAGGCAATCATCAGGTCGTGACGGGCACCGAGAGAAAACHTGGTCTATATGCAA	2044
QY	1861	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTCGGGGTGATGAGCGGTCAATG	1920
DB	2045	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTCGGGGTGATGAGCGGTCAATG	2104
QY	1921	CCCCTCTTCATGAGCTGGCGCTGGATTCTACTCAGTGGCTGTGATCATCAAGGGATCGT	1980
DB	2105	CCCCTCTTCATGAGCTGGCGCTGGATTCTACTCAGTGGCTGTGATCATCAAGGGATCGT	2164
QY	1981	TATGAGAAGGAGGCACGGCTGAAAGAGACCATCGCGATCATGGGCTGGACACAGCAT	2040
DB	2165	TATGAGAAGGAGGCACGGCTGAAAGAGACCATCGCGATCATGGGCTGGACACAGCAT	2224
QY	2041	CTCTGGTTTACGTGGTTTCATTAGTAGCTCATCTTCCTCTTGTGAGCGCTGGCCTGCT	2100
DB	2225	CTCTGGTTTACGTGGTTTCATTAGTAGCTCATCTTCCTCTTGTGAGCGCTGGCCTGCT	2284
QY	2101	GTGTCATCTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGAATCCACGGCTGGTTTGT	2160
DB	2285	GTGTCATCTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGAATCCACGGCTGGTTTGT	2344
QY	2161	TTCTGTCCGTGTTTGTGTGTTGATGCAATCTCTGCAGTCTTCCTGATTGACACACTCTT	2220
DB	2345	TTCTGTCCGTGTTTGTGTGTTGATGCAATCTCTGCAGTCTTCCTGATTGACACACTCTT	2404
QY	2221	TCCAGAGCAACCTGCGACAGCCTGTGGGGGCATCTACTTTCACGCTGACTTGCCT	2280
DB	2405	TCCAGAGCAACCTGCGACAGCCTGTGGGGGCATCTACTTTCACGCTGACTTGCCT	2464
QY	2281	TAGTCTCTGTGTGTCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAG	2340
DB	2465	TAGTCTCTGTGTGTCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAG	2524
QY	2341	CTGCTGTCTCTGTGCTTTTGGGTTTGGCTGTAGTACTTTGCCCTTTTGGAGGACAG	2400
DB	2525	CTGCTGTCTCTGTGCTTTTGGGTTTGGCTGTAGTACTTTGCCCTTTTGGAGGACAG	2584
QY	2401	GGCATTGGAGTGCAGTGGGACACCTGTTTGAGAGTCCGTGTGGAGGAAGATGGCTCAAT	2460
DB	2585	GGCATTGGAGTGCAGTGGGACACCTGTTTGAGAGTCCGTGTGGAGGAAGATGGCTCAAT	2644
QY	2461	CTCACCACITCGATCTCCATGATGTGTTTGACACCTTCCTCTATGSGGTGATGACCTGG	2520
DB	2645	CTCACCACITCGGTCTCCATGATGTGTTTGACACCTTCCTCTATGSGGTGATGACCTGG	2704
QY	2521	TACATTGAGCTGTCTTTCCAGGCCAGTACGGAATTCCTCAGGCGCTGGTATTTCCCTGG	2580
DB	2705	TACATTGAGCTGTCTTTCCAGGCCAGTACGGAATTCCTCAGGCGCTGGTATTTCCCTGG	2764
QY	2581	ACCAAGTCTCTACTGGTTTGGGAGGAAAGTGTGAGAGAGCCACCTGGTTCACACCCAG	2640
DB	2765	ACCAAGTCTCTACTGGTTTGGGAGGAAAGTGTGAGAGAGCCACCTGGTTCACACCCAG	2824
QY	2641	AAGAGAAATGTCAAAATCTGCATGAGGAGAACCCACCCACTTGAAGCTGGCGGTGCT	2700
DB	2825	AAGAGAAATGTCAAAATCTGCATGAGGAGAACCCACCCACTTGAAGCTGGCGGTGCT	2884
QY	2701	ATTCAAGAACTGGTAAAAAGTCTACCGAGATGGGATGAAGTGGCTGTGCGATGGCCTGGCA	2760
DB	2885	ATTCAAGAACTGGTAAAAAGTCTACCGAGATGGGATGAAGTGGCTGTGCGATGGCCTGGCA	2944
QY	2761	CTGAATTTTATGAGGGCCAGATCACCTCTCTCTGGGCCACAAATGGAGCGGGGAAGCG	2820
DB	2945	CTGAATTTTATGAGGGCCAGATCACCTCTCTCTGGGCCACAAATGGAGCGGGGAAGCG	3004
QY	2821	ACACATGTCAATCCTGACCGGGTGTGTTCCCCCGGACCTCGGGCACCGCTACATCTTG	2880

Db	3005	ACACACATGTCATCTCTGACGGGTGTTCCTCCCGACCTCGGCGCACCGCTACATCCTTG	3064
Qy	2881	GGAAAGACATTCGCTCTCAGATGACCACTCCGGCAGAACCTCGGGGTCTCTGCCCCAG	2940
Db	3065	GGAAAGACATTCGCTCTCAGATGACCACTCCGGCAGAACCTCGGGGTCTCTGCCCCAG	3124
Qy	2941	CATAAGTGCTGTTTGACATGCTGACTCTGAGAGACACATCTCTGGTTCATGCGCCGCTTG	3000
Db	3125	CATAAGTGCTGTTTGACATGCTGACTCTGAGAGACACATCTCTGGTTCATGCGCCGCTTG	3184
Qy	3001	AAAGGGCTCTCTGAGAGCACGCTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTGGT	3060
Db	3185	AAAGGGCTCTCTGAGAGCACGCTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTGGT	3244
Qy	3061	TTGCCATCAAGCAAGCTGAAAAACAAACAGCCAGCTGTCTAGGTGGAATGCAGAGAAAG	3120
Db	3245	TTGCCATCAAGCAAGCTGAAAAACAAACAGCCAGCTGTCTAGGTGGAATGCAGAGAAAG	3304
Qy	3121	CTATCTGTGGCCCTTGCGCCCTTCTCGGGGATCTTAAGGTGTTCATCTCTGGATGAACCCACA	3180
Db	3305	CTATCTGTGGCCCTTGCGCCCTTCTCGGGGATCTTAAGGTGTTCATCTCTGGATGAACCCACA	3364
Qy	3181	GCTGGTGTGGACCTTACTCCCGCAGGGGAAATATGGGAGCTGTCTGAAATACCGACAA	3240
Db	3365	GCTGGTGTGGACCTTACTCCCGCAGGGGAAATATGGGAGCTGTCTGAAATACCGACAA	3424
Qy	3241	GGCGGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCCTGGGGACAGG	3300
Db	3425	GGCGGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCCTGGGGACAGG	3484
Qy	3301	ATTGCCATCATCTCCCATGGGAAGTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAAGAC	3360
Db	3485	ATTGCCATCATCTCCCATGGGAAGTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAAGAC	3544
Qy	3361	CAGCTGGGAACAGGCTACTACCTGTGCTCAGGAAGATGTGGAATCCTCCCTCAGT	3420
Db	3545	CAGCTGGGAACAGGCTACTACCTGTGCTCAGGAAGATGTGGAATCCTCCCTCAGT	3604
Qy	3421	TCCTGCGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTCFCAG	3480
Db	3605	TCCTGCGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTCFCAG	3664
Qy	3481	AGCAGTTCTGATGCTGGCTGGGACGACACCATGAGATGACACGCTGACCATCGATGTC	3540
Db	3665	AGCAGTTCTGATGCTGGCTGGGACGACACCATGAGATGACACGCTGACCATCGATGTC	3724
Qy	3541	TCCTGCTATCTCCAACCTCATCAGGAGCATGTGCTGAGCCCGGCTGGTGGAGACATA	3600
Db	3725	TCCTGCTATCTCCAACCTCATCAGGAGCATGTGCTGAGCCCGGCTGGTGGAGACATA	3784
Qy	3601	GGGCATGAGCTGACCTATGTCTGGCATATGAAGCTGCTAAGGAGGAGGACCTTTGTGAA	3660
Db	3785	GGGCATGAGCTGACCTATGTCTGGCATATGAAGCTGCTAAGGAGGAGGACCTTTGTGAA	3844
Qy	3661	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTTGGGCATTTCTAGTTATGGCATCTCA	3720
Db	3845	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTTGGGCATTTCTAGTTATGGCATCTCA	3904
Qy	3721	GAGACGACCTTGGAAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG	3780
Db	3905	GAGACGACCTTGGAAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG	3964
Qy	3781	ACCTTCAGATGGTACCTTTGCCAGACAGCAAAACAGCGGGGCTTCGGGGGACACAGCAGC	3840
Db	3965	ACCTTCAGATGGTACCTTTGCCAGACAGCAAAACAGCGGGGCTTCGGGGGACACAGCAGC	4024
Qy	3841	TGCTCTCGCCGTTCACTGAAGATGATGCTGCTGATCAAAATGATCTTGACATAGACCCA	3900
Db	4025	TGCTCTCGCCGTTCACTGAAGATGATGCTGCTGATCAAAATGATCTTGACATAGACCCA	4084
Qy	3901	GAATCCAGAGACAGACTTGCTCAGTGGGATGGATGGCAAGGGTCTCTACAGGTGAAA	3960

QY 5041 GTCAGCAAGCAACACCTGAGTTCATCAGTGAAGCCCTGTCATCTACTGGCTC 5100
Db 5225 GTCAGCAAGCAACACACCTGAGTTCATCAGTGAAGCCCTGTCATCTACTGGCTC 5284
QY 5101 TCTAATTTTGTCTGGGATATGTGCAATACGTTGTCCCTGCCACACTGGTCAATATCATC 5160
Db 5285 TCTAATTTTGTCTGGGATATGTGCAATACGTTGTCCCTGCCACACTGGTCAATATCATC 5344
QY 5161 TTCATCTGCTCCAGAGAAAGTCCATGTGCTCCTCCACCAATCTGCCCTGGTGAGCCCTT 5220
Db 5345 TTCATCTGCTCCAGAGAAAGTCCATGTGCTCCTCCACCAATCTGCCCTGGTGAGCCCTT 5404
QY 5221 CTACTTTTCTGTATGGGTGGTCAATCAACCTCTCATGTACCCAGCCCTCTTTGTGTTTC 5280
Db 5405 CTACTTTTCTGTATGGGTGGTCAATCAACCTCTCATGTACCCAGCCCTCTTTGTGTTTC 5464
QY 5281 AAGATCCCAGACAGCCCTATGTGTGCTCAGCGCTGTTCCAGCAATAGCTGAATATATCAAT 5340
Db 5465 AAGATCCCAGACAGCCCTATGTGTGCTCAGCGCTGTTCCAGCAATAGCTGAATATATCAAT 5524
QY 5341 GGCAGCGTGGCCACCTTTGTGCTGAGCTGTTCCAGCAATAGCTGAATATATCAAT 5400
Db 5525 GGCAGCGTGGCCACCTTTGTGCTGAGCTGTTCCAGCAATAGCTGAATATATCAAT 5584
QY 5401 GATATCCTGAAGTCCGTGTTCTTGTATCTTCCACATTTTTCGCTGGGACGAGGCTCATC 5460
Db 5585 GATATCCTGAAGTCCGTGTTCTTGTATCTTCCACATTTTTCGCTGGGACGAGGCTCATC 5644
QY 5461 GACATGGTGAAGAACCCAGGCAATGCTGATGCCCTGGAGAGTTTGGGAGAAATCGCTTT 5520
Db 5645 GACATGGTGAAGAACCCAGGCAATGCTGATGCCCTGGAGAGTTTGGGAGAAATCGCTTT 5704
QY 5521 GTGTCAACATTTATCTTGGGACTTGTGGGAGGAAACCTTCTCGCATGGCCGTGGAAGGG 5580
Db 5705 GTGTCAACATTTATCTTGGGACTTGTGGGAGGAAACCTTCTCGCATGGCCGTGGAAGGG 5764
QY 5581 GTGGTGTCTTCTCATCTACTGTTCTGATCCAGTACAGATTTCTCATCAGGCCAGAGCTT 5640
Db 5765 GTGGTGTCTTCTCATCTACTGTTCTGATCCAGTACAGATTTCTCATCAGGCCAGAGCTT 5824
QY 5641 GTAATGCAAAAGCTATCTCCTCTGAATGATGAAGATGAAGTGTGAGCGGGGAAAGACAG 5700
Db 5825 GTAATGCAAAAGCTATCTCCTCTGAATGATGAAGTGTGAGCGGGGAAAGACAG 5884
QY 5701 AGAATCTTGTATGGTGGAGGCGCAATGACATCTTGAAGATCAAGAGTGTACGAAAGATA 5760
Db 5885 AGAATCTTGTATGGTGGAGGCGCAATGACATCTTGAAGATCAAGAGTGTACGAAAGATA 5944
QY 5761 TATAGAAGGAGCGGAGCCTGCTGTTGACAGGATTTTCGTTGGGCATCTCCTCTGGTGAG 5820
Db 5945 TATAGAAGGAGCGGAGCCTGCTGTTGACAGGATTTTCGTTGGGCATCTCCTCTGGTGAG 6004
QY 5821 TGCCTTGGGCTCTCGGAGTTTAATGGGCTGSGAAATCATCAACTTTCAAGATGTTAACA 5880
Db 6005 TGCCTTGGGCTCTCGGAGTTTAATGGGCTGSGAAATCATCAACTTTCAAGATGTTAACA 6064
QY 5881 GGAGATACCATCTGTACAGAGGAGATGCTTTCCTTACAAAAATAGTATCTTATCAAC 5940
Db 6065 GGAGATACCATCTGTACAGAGGAGATGCTTTCCTTACAAAAATAGTATCTTATCAAC 6124
QY 5941 ATCCATGAATACATCAGAACATGGGCTACTGCGCTCAGTTTGTGATGCCATCAGAGAGCTG 6000
Db 6125 ATCCATGAATACATCAGAACATGGGCTACTGCGCTCAGTTTGTGATGCCATCAGAGAGCTG 6184
QY 6001 TTGACTGGAGAGAACAGCTGGAGTTCTTTGCCCTTTTGGAGAGAGTCCCGAGAGAGAA 6060
Db 6185 TTGACTGGAGAGAACAGCTGGAGTTCTTTGCCCTTTTGGAGAGAGTCCCGAGAGAGAA 6244
QY 6061 GTTGGCAAGGTTGGTGAAGTGGGCTATCGGAACTGGGCCCTCGTGAAGTATGGAGAGAAA 6120
Db 6245 GTTGGCAAGGTTGGTGAAGTGGGCTATCGGAACTGGGCCCTCGTGAAGTATGGAGAGAAA 6304

QY 6121 TATCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
Db 6305 TATCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6364
QY 6181 GCGGGGCTCTCTGTGGTGTCTTGGATGAACCCACACAGGATGGATCCCAAGCCCGG 6240
Db 6365 GCGGGGCTCTCTGTGGTGTCTTGGATGAACCCACACAGGATGGATCCCAAGCCCGG 6424
QY 6241 CGTTCTTGTGGAAATGTGCCCCTAAAGTGTGTCAGAGGGGAGATCAGTAGTGCCTTACA 6300
Db 6425 CGTTCTTGTGGAAATGTGCCCCTAAAGTGTGTCAGAGGGGAGATCAGTAGTGCCTTACA 6484
QY 6301 TCTCATAGTATGGAAGAAATGTGAAGCTCTTTCACATAGGATGCAATCATGTGTCATGGA 6360
Db 6485 TCTCATAGTATGGAAGAAATGTGAAGCTCTTTCACATAGGATGCAATCATGTGTCATGGA 6544
QY 6361 AGTTTCAGGTGCCCCTGGCAGTGTCCAGCATCTAAAAAATAGTTCGGAGATGTTTATACA 6420
Db 6545 AGTTTCAGGTGCCCCTGGCAGTGTCCAGCATCTAAAAAATAGTTCGGAGATGTTTATACA 6604
QY 6421 ATAGTTCTAGCAATAGCAGGTCACCCGAGCTGAAGCCCTGCCAGATTTCTTTTGA 6480
Db 6605 ATAGTTCTAGCAATAGCAGGTCACCCGAGCTGAAGCCCTGCCAGATTTCTTTTGA 6664
QY 6481 CTTCATTTCTCGAAGTGTCTTAAAAAGAGAAACACCGGAACATGCTACAATACCACTT 6540
Db 6665 CTTCATTTCTCGAAGTGTCTTAAAAAGAGAAACACCGGAACATGCTACAATACCACTT 6724
QY 6541 CCATCTTCATTTCTCTCTGCGCAGGATATTGAGCATCTCTCCAGAGCAAAAGCGA 6600
Db 6725 CCATCTTCATTTCTCTCTGCGCAGGATATTGAGCATCTCTCCAGAGCAAAAGCGA 6784
QY 6601 CTCACATAGAAGACTACTCTGTTCTCAGACAACTTGAACCAAGTATTGTTGAACTTT 6660
Db 6785 CTCACATAGAAGACTACTCTGTTCTCAGACAACTTGAACCAAGTATTGTTGAACTTT 6844
QY 6661 GCMAGGACCAAGTATGATGACCACTTAAAAAGACTCTCATTACAAAAACCAAGACA 6720
Db 6845 GCMAGGACCAAGTATGATGACCACTTAAAAAGACTCTCATTACAAAAACCAAGACA 6904
QY 6721 GTAGTGACCTTGCAGTCTCAGATCTTTCACAGATGAGAAAGTGAAGAAAGCTAT 6780
Db 6905 GTAGTGACCTTGCAGTCTCAGATCTTTCACAGATGAGAAAGTGAAGAAAGCTAT 6964
QY 6781 GTAT 6784
Db 6965 GTAT 6968

RESULT 13

AAS06121
ID AAS06121 standard; cDNA; 9854 BP.

XX AAS06121;
XX AC AC
XX XX
DT 12-SEP-2001 (first entry)
XX Human ABC1 DNA sequence #2.
DE Human; ABC1 gene; atherosclerosis; reverse transport; cholesterol;
KW cardiovascular; neurological; Tangier disease; LCAT deficiency;
KW lecithin-cholesterol acetyltransferase; malaria; diabetes; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 298..7078
FT /tag= a
FT /product= "Human ABC1 protein"
PN WO200130848-A2.
XX 03-MAY-2001.
PD

XX 26-OCT-2000; 2000WO-EF10886.
 XX 26-OCT-1999; 99EP-0402668.
 PR 01-MAR-2000; 2000US-0186260.
 XX (AVET) AVENTIS PHARMA SA.
 PA Denefle P, Rosier-Montus M, Arnould-Requigne I, Prades C, Naudin L;
 PI Lemoline C, Duverger N, Jaye M, Searfoss GH, Remaley A, Brewer HB;
 PI Dean M;
 XX WPI; 2001-316327/33.
 DR P-PSDB; AAU02176.
 XX New human ABC1 nucleic acids and polypeptides for treating
 PT atherosclerosis, malaria and diabetes -
 XX Claim 1: Page 209-213; 368pp; English.
 CC The sequence represents the coding sequence #2 of human ABC1. The
 CC nucleic acid sequence, primers and probes derived from the ABC1 sequence,
 CC and polypeptides and vectors are useful for the prevention of
 CC atherosclerosis, in a subject affected by a dysfunction in the reverse
 CC transport of cholesterol. The polypeptide encoded by the ABC1 gene is
 CC useful for screening for an active ingredient for the prevention or
 CC treatment of a disease resulting from dysfunction in the reverse
 CC transport of cholesterol. The nucleic acids and polypeptides are also
 CC useful for treating and preventing cardiovascular and neurological
 CC pathologies, and other diseases e.g. Tangier disease, lecithin-
 CC cholesterol (LCAT) deficiency, malaria and diabetes.
 XX Sequence 9854 BP; 2665 A; 2219 C; 2334 G; 2635 T; 1 other;
 SQ

Query Match 99.7%; Score 6764.8; DB 22; Length 9854;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

1 ATGGCTGTGGCTCAGCTGAGTGTCTGCTGTGGAAGACCTCACTTTCAGAAAGA 60
 298 ATGGCTGTGGCTCAGCTGAGTGTCTGCTGTGGAAGACCTCACTTTCAGAAAGA 357
 61 CAACATGTGAGTGTCTGAGTGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 120
 358 CAACATGTGAGTGTCTGAGTGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 417
 121 TCTGTGGCTGAGTGTCTGAGTGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 180
 418 TCTGTGGCTGAGTGTCTGAGTGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 477
 181 ATGGCTGTGAGTGTCTGAGTGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 240
 478 ATGGCTGTGAGTGTCTGAGTGTGGCTGCTCTATTTATCTTCCTGATCCTGATC 537
 241 TGTTCGTTTACCGACTCTGGGAGGCTCCCGGAGTGTGGGAACTTTACAAATCC 300
 538 TGTTCGTTTACCGACTCTGGGAGGCTCCCGGAGTGTGGGAACTTTACAAATCC 597
 301 ATGTGGCTGCGCTGTCTCAGATGTCTGAGGCTTCTTTTATACAGCCAGAAAGACAC 360
 598 ATGTGGCTGCGCTGTCTCAGATGTCTGAGGCTTCTTTTATACAGCCAGAAAGACAC 657
 361 AGCATGAAGACATCGGCAAGTTCAGAACTTACAGAGATCAAGAAATCCAGCTCA 420
 658 AGCATGAAGACATCGGCAAGTTCAGAACTTACAGAGATCAAGAAATCCAGCTCA 717
 421 AACTTGAAGCTTCAAGATTCCTGGTGGACATGAACCTTCTCTGGTTCCTATATCAC 480
 718 AACTTGAAGCTTCAAGATTCCTGGTGGACATGAACCTTCTCTGGTTCCTATATCAC 777
 481 AACTTCTCTCCCAAGTCTACTGTGGACAGATGCTGAGGCTGATGTCATCTCCAC 540
 778 AACTTCTCTCCCAAGTCTACTGTGGACAGATGCTGAGGCTGATGTCATCTCCAC 837

QY 541 AAGGATATTTTCAAGGCTACCAAGTTCATATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
 DB 838 AAGGATATTTTCAAGGCTACCAAGTTCATATTTGACAAGTCTGTGCAATGGATCAAAATCA 897
 QY 601 GAAGAGATGATTAACACTTGGTGACCAAGAGTTTCTGAGCTTTTGGGCTACCAAGAGAG 660
 DB 898 GAAGAGATGATTAACACTTGGTGACCAAGAGTTTCTGAGCTTTTGGGCTACCAAGAGAG 957
 QY 661 AACTGGCTGACAGAGAGGAGTACTTCTGTCACATGGACATCCTGAAGCAATCTCTG 720
 DB 958 AACTGGCTGACAGAGAGGAGTACTTCTGTCACATGGACATCCTGAAGCAATCTCTG 1017
 QY 721 AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGAGTGTGGCTGAAGCCACAAATAACA 780
 DB 1018 AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGAGTGTGGCTGAAGCCACAAATAACA 1077
 QY 781 TTGCTGCATAGTCTTGGGACTCTGCCAGAGAGCTGTTCAGCATGAGAAGCTGGAGTGAC 840
 DB 1078 TTGCTGCATAGTCTTGGGACTCTGCCAGAGAGCTGTTCAGCATGAGAAGCTGGAGTGAC 1137
 QY 841 ATGCACAGAGAGTGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCCTCCACCCAAATC 900
 DB 1138 ATGCACAGAGAGTGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCCTCCACCCAAATC 1197
 QY 901 TACCAGGCTGTCTCGTATTTCTGCGGGCATCCCGAGGAGGGGGCTGAGATCAAG 960
 DB 1198 TACCAGGCTGTCTCGTATTTCTGCGGGCATCCCGAGGAGGGGGCTGAGATCAAG 1257
 QY 961 TCTCTCAACTGCTATGAGGACAACTTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
 DB 1258 TCTCTCAACTGCTATGAGGACAACTTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1317
 QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTCTTACTGCAATGATTTGATGAAG 1080
 DB 1318 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTCTTACTGCAATGATTTGATGAAG 1377
 QY 1081 AATTTGGAGTCTAGTCTCTTTCCCGCATTTCTGAAAGCTCTGAAGCCGCTGCTCGTT 1140
 DB 1378 AATTTGGAGTCTAGTCTCTTTCCCGCATTTCTGAAAGCTCTGAAGCCGCTGCTCGTT 1437
 QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACCAAGCAGTCAATGGCTGAGTGAAC 1200
 DB 1438 GGAAGATCCTGTATACACTGACACTCCAGCCACCAAGCAGTCAATGGCTGAGTGAAC 1497
 QY 1201 AAGACTTCCAGGAACTGGCTGTGTCCATGATCTGGAAGGATCTGGGAGGAACTCAGC 1260
 DB 1498 AAGACTTCCAGGAACTGGCTGTGTCCATGATCTGGAAGGATCTGGGAGGAACTCAGC 1557
 QY 1261 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1320
 DB 1558 CCCAAGATCTGGACCTTCATGGAGAACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1617
 QY 1321 GACAGCAGGACAATGACACCTTTTGGGAAACAGAGTGTGGATGGCTTAGATTGGACAGCC 1380
 DB 1618 GACAGCAGGACAATGACACCTTTTGGGAAACAGAGTGTGGATGGCTTAGATTGGACAGCC 1677
 QY 1381 CAAGACATCGTGGCGTTTGGCCCAAGCACCAGAGGATGTCCAGTCCAGTAAATGGTTCT 1440
 DB 1678 CAAGACATCGTGGCGTTTGGCCCAAGCACCAGAGGATGTCCAGTCCAGTAAATGGTTCT 1737
 QY 1441 GTGTACACCTGGAGAGAGCTTTTCAACAGAGTAAACAGGCAATCCGGACCAATATCTGCG 1500
 DB 1738 GTGTACACCTGGAGAGAGCTTTTCAACAGAGTAAACAGGCAATCCGGACCAATATCTGCG 1797
 QY 1501 TTTATGGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1560
 DB 1798 TTTATGGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1857
 QY 1561 AACAAGTCCATGGAGCTGCTGGATGAGAGGAAATTTCTGGGCTGGTATTGTGTTCACTGGA 1620
 DB 1858 AACAAGTCCATGGAGCTGCTGGATGAGAGGAAATTTCTGGGCTGGTATTGTGTTCACTGGA 1917

QY 1621 ATTACTCCAGGAGCAATTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATT 1680
 Db 1918 ATTACTCCAGGAGCAATTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATT 1977
 QY 1681 GACAAATGTGGAGAGCAAAATAAATCAAGATGGGTACTGGGACCTGGTCTCGAGCT 1740
 Db 1978 GACAATGTGGAGAGCAAAATAAATCAAGATGGGTACTGGGACCTGGTCTCGAGCT 2037
 QY 1741 GACCCCTTTGAGGACATGCGTACGTCCTGGGGGCTTCCGCTACTTCGAGGATGGTG 1800
 Db 2038 GACCCCTTTGAGGACATGCGTACGTCCTGGGGGCTTCCGCTACTTCGAGGATGGTG 2097
 QY 1801 GAGCAGCAATCATGAGGTGCTGAGCGGCACCGAGAGAAAACCTGGTCTATATGCAA 1860
 Db 2098 GAGCAGCAATCATGAGGTGCTGAGCGGCACCGAGAGAAAACCTGGTCTATATGCAA 2157
 QY 1861 CAGATGCCCTATCCCTGTTACCTTGATGACATCTTCTGCGGGTGTAGCGCGGTCAATG 1920
 Db 2158 CAGATGCCCTATCCCTGTTACCTTGATGACATCTTCTGCGGGTGTAGCGCGGTCAATG 2217
 QY 1921 CCCCTCTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 1980
 Db 2218 CCCCTCTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGTG 2277
 QY 1981 TATGAGAGGAGCAGCGCTGAAGAGACCATGGGATCATGGGCTGGACAAAGCATA 2040
 Db 2278 TATGAGAGGAGCAGCGCTGAAGAGACCATGGGATCATGGGCTGGACAAAGCATA 2337
 QY 2041 CTCCTGTTAGCTGGTTCATTAGTAGACCTTCCTCTCTTGTGAGCGCTGGCCCTGCTA 2100
 Db 2338 CTCCTGTTAGCTGGTTCATTAGTAGACCTTCCTCTCTTGTGAGCGCTGGCCCTGCTA 2397
 QY 2101 GTGGTCATCCTGAAGTAGGAACCTGTCGCCCTACAGTATCCAGCGTGGTGTGTC 2160
 Db 2398 GTGGTCATCCTGAAGTAGGAACCTGTCGCCCTACAGTATCCAGCGTGGTGTGTC 2457
 QY 2161 TTCCTGTCGCTGTTGCTGTGGTGACATCTTCGAGTGTCTCTGATGACACATCTTC 2220
 Db 2458 TTCCTGTCGCTGTTGCTGTGGTGACATCTTCGAGTGTCTCTGATGACACATCTTC 2517
 QY 2221 TCAGAGCAACCTGGCAGCAGCCTGTGGGGCATCATCTACTTACCGCTGACCTGGCC 2280
 Db 2518 TCAGAGCAACCTGGCAGCAGCCTGTGGGGCATCATCTACTTACCGCTGACCTGGCC 2577
 QY 2281 TAGCTCCTGTGTGGCATGGCAGACTACGTGGCTTCACACTCAAGATCTTCGCTAGC 2340
 Db 2578 TAGCTCCTGTGTGGCATGGCAGACTACGTGGCTTCACACTCAAGATCTTCGCTAGC 2637
 QY 2341 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGAGCAG 2400
 Db 2638 CTGCTGTCTCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGAGCAG 2697
 QY 2401 GGCATTGAGTGCAGTGGAGCAACCTGTTGAGAGTCTGTGGAGAGAGATGGCTTCAAT 2460
 Db 2698 GGCATTGAGTGCAGTGGAGCAACCTGTTGAGAGTCTGTGGAGAGAGATGGCTTCAAT 2757
 QY 2461 CTCACACATTCGATCTCCATGATGCTGTTGACACCTTCTCTATGGGGTGATGACCTGG 2520
 Db 2758 CTCACACATTCGATCTCCATGATGCTGTTGACACCTTCTCTATGGGGTGATGACCTGG 2817
 QY 2521 TACATTGAGGCTGTCTTTCCAGCCAGTACCGAATTCAGGCGCTGGTATTTCCCTTGC 2580
 Db 2818 TACATTGAGGCTGTCTTTCCAGCCAGTACCGAATTCAGGCGCTGGTATTTCCCTTGC 2877
 QY 2581 ACCAAGTCTACTGTTTGGCGAGAAAGTGTATGAGAGAGCAGCCCTGGTTCACACAG 2640
 Db 2878 ACCAAGTCTACTGTTTGGCGAGAAAGTGTATGAGAGAGCAGCCCTGGTTCACACAG 2937
 QY 2641 AAGAGAAATCAGAAATCTGATGAGAGGAAACCCACCTTGAAGCTGGCGGTGCC 2700
 Db 2938 AAGAGAAATCAGAAATCTGATGAGAGGAAACCCACCTTGAAGCTGGCGGTGCC 2997
 QY 2701 ATTACAGACCTGGTAAAGTCTACCGAGATGGATGAAGGCTGCTGATGGCGCTGSCA 2760

Db 2998 ATTACAGACCTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGCGATGSCCTGGCA 3057
 QY 2761 CTGAATTTTATGAGGGCCAGATCACCTCTCTTCTGGGCCACAAATGAGCGGGAGAGCG 2820
 Db 3058 CTGAATTTTATGAGGGCCAGATCACCTCTCTTCTGGGCCACAAATGAGCGGGAGAGCG 3117
 QY 2821 ACCACCATGTCAATCTGACCGGGTGTTCCTCCCGGACCTCGGSCACCCCTACATCCTG 2880
 Db 3118 ACCACCATGTCAATCTGACCGGGTGTTCCTCCCGGACCTCGGSCACCCCTACATCCTG 3177
 QY 2881 GGAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG 2940
 Db 3178 GGAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG 3237
 QY 2941 CATACGCTGTGTTGACATGCTGACCTGCTCGAAGAACACATCTGGTCTATGCCCGCTTG 3000
 Db 3238 CATACGCTGTGTTGACATGCTGACCTGCTCGAAGAACACATCTGGTCTATGCCCGCTTG 3297
 QY 3001 AAGGGCTCTCTGAGAACGCTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3060
 Db 3298 AAGGGCTCTCTGAGAACGCTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3357
 QY 3061 TTGCCATCAAGCAGCTGAAGAACAAACAAACAGCCAGCTGTCAAGTGAATGCAGAGAAAG 3120
 Db 3358 TTGCCATCAAGCAGCTGAAGAACAAACAAACAGCCAGCTGTCAAGTGAATGCAGAGAAAG 3417
 QY 3121 CTATCTGTGGGCTTTGTCGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA 3180
 Db 3418 CTATCTGTGGGCTTTGTCGGGGATCTAAGGTTGTCATTCTGGATGAACCCACA 3477
 QY 3181 GCTGGTGTGACCTTACTCCCGAGGGGAATATGGAGCTGTCTGTGAATACCGACAA 3240
 Db 3478 GCTGGTGTGACCTTACTCCCGAGGGGAATATGGAGCTGTCTGTGAATACCGACAA 3337
 QY 3241 GGCGCACCATTATCTCTCTACACACCATGATGAAGCGAGCTCTCGGGGACAGG 3300
 Db 3358 GGCGCACCATTATCTCTCTACACACCATGATGAAGCGAGCTCTCGGGGACAGG 3397
 QY 3301 ATTGCCATCATCTCCATGGGAAGCTGTGTGTGGGCTCTCCCTGTTTCTGAAGAAC 3360
 Db 3598 ATTGCCATCATCTCCATGGGAAGCTGTGTGTGGGCTCTCCCTGTTTCTGAAGAAC 3657
 QY 3361 CAGCTGGAAACAGGCTACTACTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3420
 Db 3658 CAGCTGGAAACAGGCTACTACTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT 3717
 QY 3421 TCCTGCAGAAACAGTAGTACCTGTGTCTATACCTGAAAAGAGGAGACAGTGTCTCAG 3480
 Db 3718 TCCTGCAGAAACAGTAGTACCTGTGTCTATACCTGAAAAGAGGAGACAGTGTCTCAG 3777
 QY 3481 AGCAGTTCTGATGCTGGCTGGGAGCAGCATGAGAGTACAGGCTGACCATCGATGTC 3540
 Db 3778 AGCAGTTCTGATGCTGGCTGGGAGCAGCATGAGAGTACAGGCTGACCATCGATGTC 3837
 QY 3541 TCTGCTATCTCCACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGTGTGGAAGACATA 3600
 Db 3838 TCTGCTATCTCCACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGTGTGGAAGACATA 3897
 QY 3601 GGGCATGAGCTGACCTATGTGCTGCCATATGAGCTGCTTAGGAGGAGGAGCTTTTGGAA 3660
 Db 3898 GGGCATGAGCTGACCTATGTGCTGCCATATGAGCTGCTTAGGAGGAGGAGCTTTTGGAA 3957
 QY 3661 CTCCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTTATGGCATCTCA 3720
 Db 3958 CTCCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTTATGGCATCTCA 4017
 QY 3721 GAGAGACCTCTGGAAGAAATATTCCTCAAGGTGGCCGAGAGAGTGGGTGGATGCTGAG 3780
 Db 4018 GAGAGACCTCTGGAAGAAATATTCCTCAAGGTGGCCGAGAGAGTGGGTGGATGCTGAG 4077
 QY 3781 ACCTCAGATGCTACCTTGCAGCAAGACAGAAACAGGGGCGCTTCGGGGGACAGAGAGC 3840

Db 4078 ACCTCAGATGGTACCTTGGCAGCAAGCAAGAACAGCGCGGCTTGGGGACAAGCAGAGC 4137
QY 3841 TGTCTTCGCCCGCTTCACTGAAGATGATGCTGTGATCCAAATGATCTCAGATAGACCCA 3900
Db 4138 TGTCTTCGCCCGCTTCACTGAAGATGATGCTGTGATCCAAATGATCTCAGATAGACCCA 4197
QY 3901 GAATCCAGAGACAGACTTGTCTCACTGGGATGGATGGCAAGGGTCCCTACCAGGTGAAA 3960
Db 4198 GAATCCAGAGACAGACTTGTCTCACTGGGATGGATGGCAAGGGTCCCTACCAGGTGAAA 4257
QY 3961 GGCTGGAATCTTACACAGAACAGTTGTGGCCCTTTTGTGGAAGAGATGCTTAATGGCC 4020
Db 4258 GGCTGGAATCTTACACAGAACAGTTGTGGCCCTTTTGTGGAAGAGATGCTTAATGGCC 4317
QY 4021 AGACGGAGTCGGAAGAGATTTTGTCTCAGATTGTCTGCCAGCTGTGTTTGTCTGCATT 4080
Db 4318 AGACGGAGTCGGAAGAGATTTTGTCTCAGATTGTCTGCCAGCTGTGTTTGTCTGCATT 4377
QY 4081 GCCCTTGTGTCTCAGCTGATGCTGCCACCCCTTTGGCAAGTACCCCAAGCTGGAACCTCAG 4140
Db 4378 GCCCTTGTGTCTCAGCTGATGCTGCCACCCCTTTGGCAAGTACCCCAAGCTGGAACCTCAG 4437
QY 4141 CCCTGTGATGTACAAACAGATACACATTTGTCCAGCAATGTGTCAGCAATGTGCTCCTCAGGACAGGGA 4200
Db 4438 CCCTGTGATGTACAAACAGATACACATTTGTCCAGCAATGTGCTCCTCAGGACAGGGA 4497
QY 4201 ACCCTGGAATCTTTAAACGCCCTTCAACAAAGACCCCTGCTTGGGACCCGCTGTATGGAA 4260
Db 4498 ACCCTGGAATCTTTAAACGCCCTTCAACAAAGACCCCTGCTTGGGACCCGCTGTATGGAA 4557
QY 4261 GGAACCCCAATCCCAACAGCCCTGCCAGGACAGGAGGAGAGATGACCACTGCCCA 4320
Db 4558 GGAACCCCAATCCCAACAGCCCTGCCAGGACAGGAGGAGATGACCACTGCCCA 4617
QY 4321 GTTCCCAAGACCATCATGACACCTTCTCCAGATGGGAATGACAAATGCAGAACCTTCA 4380
Db 4618 GTTCCCAAGACCATCATGACACCTTCTCCAGATGGGAATGACAAATGCAGAACCTTCA 4677
QY 4381 CTTGCAATGCCAGTGTAGCAGCGCAAAATCAAGAAGATGCTGCTGTGTCCCCAGGG 4440
Db 4678 CTTGCAATGCCAGTGTAGCAGCGCAAAATCAAGAAGATGCTGCTGTGTCCCCAGGG 4737
QY 4441 GCAGGGGGCTGCTCCTCCACAAAGAAACAAACACATGCAGATATCTTCAGGACCTG 4500
Db 4738 GCAGGGGGCTGCTCCTCCACAAAGAAACAAACACATGCAGATATCTTCAGGACCTG 4797
QY 4501 ACAGGAAGAAACATTTCCGATTAATCTGGTGAAGACGTATGTCCAGATCATAGCCAAAGC 4560
Db 4798 ACAGGAAGAAACATTTCCGATTAATCTGGTGAAGACGTATGTCCAGATCATAGCCAAAGC 4857
QY 4561 TTAAGACAGATCTGGGTGATGATTTAGTATGGCGGCTTTCCCTGGGTGTCAGT 4620
Db 4858 TTAAGACAGATCTGGGTGATGATTTAGTATGGCGGCTTTCCCTGGGTGTCAGT 4917
QY 4621 AATACTCAAGCACTTCCCTCCGAGTCAAGAGTTAATGATGCCATCAACAAATGAAGAAA 4680
Db 4918 AATACTCAAGCACTTCCCTCCGAGTCAAGAGTTAATGATGCCACCAACAAATGAAGAAA 4977
QY 4681 CACCTAAGCTGCCAAGACAGTCTTCAGATCGATTTCTCAACAGCTTGGAGATTT 4740
Db 4978 CACCTAAGCTGCCAAGACAGTCTTCAGATCGATTTCTCAACAGCTTGGAGATTT 5037
QY 4741 ATGACAGGACTGGACACCAAGAAATATGTCAAGGTGTGGTTCAATAAAGGCTGGCAT 4800
Db 5038 ATGACAGGACTGGACACCAAGAAATATGTCAAGGTGTGGTTCAATAAAGGCTGGCAT 5097
QY 4801 GCAATCAGCTCTTCTGATGATCATCAACATGCAATGCAATTTCTCCGGGCCCAACCTGCAAAAG 4860
Db 5098 GCAATCAGCTCTTCTGATGATCATCAACATGCAATGCAATTTCTCCGGGCCCAACCTGCAAAAG 5157
QY 4861 GGAGAGACCTTAGCCATATGAAATTTACTGCTTTTCAATCATCCCTGATCTCACCAG 4920
Db 5158 GGAGAGACCTTAGCCATATGAAATTTACTGCTTTTCAATCATCCCTGATCTCACCAG 5217

QY 4921 CAGCAGCTCTCAGAGGTGGCTCTGATGACCACATCAGTGGATGCTCTTGTGTCCATCTGT 4980
Db 5218 CAGCAGCTCTCAGAGGTGGCTCCGATGACCATCAGTGGATGCTCTTGTGTCCATCTGT 5277
QY 4981 GTCACTCTTGAATGCTCTGCTCCAGCCAGCTTGTGCTGATTTGCTGATCCAGAGCGG 5040
Db 5278 GTCACTCTTGAATGCTCTGCTCCAGCCAGCTTGTGCTGATTTGCTGATCCAGAGCGG 5337
QY 5041 GTCACAAAGCAAAACACCTGCAGTTCATGAGTGGAGTGAAGCCTGTCACTACTGGCTC 5100
Db 5338 GTCACAAAGCAAAACACCTGCAGTTCATGAGTGGAGTGAAGCCTGTCACTACTGGCTC 5397
QY 5101 TCTAATTTTGTCTGGGATATGCAATTTAGCTTGTCCCTGCCACACTGGTCAATATCATC 5160
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QY 5161 TTTCACTCTGCTTCCAGCAGAAAGTCTATGTGCTCTCCACCAATCTGCTGTGCTAGCCCTT 5220
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QY 5221 CTACTTTTGTCTATGGGTGGTCAATCAGCTCTCATGTACCCAGCCTCTCTTGTGTTC 5280
Db 5518 CTACTTTTGTCTATGGGTGGTCAATCAGCTCTCATGTACCCAGCCTCTCTTGTGTTC 5577
QY 5281 AAGATCCCCAGCAGCAGCCTATGTGCTCTACACAGCTGAACCTCTTCATTGGCATTAAT 5340
Db 5578 AAGATCCCCAGCAGCAGCCTATGTGCTCTACACAGCTGAACCTCTTCATTGGCATTAAT 5637
QY 5341 GGCAGCTGGCCACCTTTGTGCTGGAGCTGTACCCGACATAAGCTGAATAATTAATCAAT 5400
Db 5638 GGCAGCTGGCCACCTTTGTGCTGGAGCTGTACCCGACATAAGCTGAATAATTAATCAAT 5697
QY 5401 GATATCTCTGAAGTCTGCTTCTGATCTTCCACATTTTGGCTGGGACGAGGCTCATC 5460
Db 5698 GATATCTCTGAAGTCTGCTTCTGATCTTCCACATTTTGGCTGGGACGAGGCTCATC 5757
QY 5461 GACATGGTGAAGAAACAGCAGTATGCTGATGCTTGAAGAGTTTGGGAGAGTTCGCTTT 5520
Db 5758 GACATGGTGAAGAAACAGCAGTATGCTGATGCTTGAAGAGTTTGGGAGAGTTCGCTTT 5817
QY 5521 GTGTCAACATTAATCTTGGGACCTTGGGACGAGAAACCTCTTGGCATGGCGTGAAGGG 5580
Db 5818 GTGTCAACATTAATCTTGGGACCTTGGGACGAGAAACCTCTTGGCATGGCGTGAAGGG 5877
QY 5581 GTGTGTTTCTTCCCTCAATCTACTTCTGATCCAGTACAGATTTCTCATCAGGCCACAGCT 5640
Db 5878 GTGTGTTTCTTCCCTCAATCTACTTCTGATCCAGTACAGATTTCTCATCAGGCCACAGCT 5937
QY 5641 GTAAATGCAAGCTATCTCTGATGATGAAGATGAAGATGTGAGCGGGGAAGACAG 5700
Db 5938 GTAAATGCAAGCTATCTCTGATGATGAAGATGAAGATGTGAGCGGGGAAGACAG 5997
QY 5701 AGAATTTTGTGATGGGCGGCGAGAAATGACATCTTTAGAAATCAAGGAGTTGACGAAGATA 5760
Db 5998 AGAATTTTGTGATGGGCGGCGAGAAATGACATCTTTAGAAATCAAGGAGTTGACGAAGATA 6057
QY 5761 TATAGAAGGAAGCGGAGCCTGCTGTTGACAGGATTTGGTGGGATTCCTCCTGGTGAG 5820
Db 6058 TATAGAAGGAAGCGGAGCCTGCTGTTGACAGGATTTGGTGGGATTCCTCCTGGTGAG 6117
QY 5821 TCTCTTTGGGCTCCTGGGAGTTAATGGGCTGGAATAATCAACTTTCAAGATGTTAACA 5880
Db 6118 TCTCTTTGGGCTCCTGGGAGTTAATGGGCTGGAATAATCAACTTTCAAGATGTTAACA 6177
QY 5881 GGAGATACCACTGTTTACCAGAGGAGATGCTTTCTTTTAAACAAAATAGTATCTTATCAAC 5940
Db 6178 GGAGATACCACTGTTTACCAGAGGAGATGCTTTCTTTTAAACAAAATAGTATCTTATCAAC 6237
QY 5941 ATCCATGAGTACATCAGAACATGGCTACTGCTCTGATGCTGATGCTGATGCTGATGCTG 6000
Db 6238 ATCCATGAGTACATCAGAACATGGCTACTGCTCTGATGCTGATGCTGATGCTGATGCTGATGCTG 6297

QY	6001	TTGACTGGGAGAGAACACGTGGAGTCTCTTGCCCTCTTTGAGAGGAGTCCGAGAGAAAGAA	6060
Db	6298	TTGACTGGGAGAGAACACGTGGAGTCTCTTGCCCTCTTTGAGAGGAGTCCGAGAGAAAGAA	6357
QY	6061	GTTGGCAAGTTGGTGAATGGGCCATTTCGGAACCTGGGCTCGTGAAGTATGGAGAAAAA	6120
Db	6358	GTTGGCAAGTTGGTGAATGGGCCATTTCGGAACCTGGGCTCGTGAAGTATGGAGAAAAA	6417
QY	6121	TATGCTGTGTAACATATAGTGGAGGCAACAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6418	TATGCTGTGTAACATATAGTGGAGGCAACAACAAGCTCTCTACAGCCATGGCTTTGATC	6477
QY	6181	GGCGGGCCCTGCTGGTGTCTCTGGATGAACCCACACAGGCATGGATCCCAAGCCCGG	6240
Db	6478	GGCGGGCCCTGCTGGTGTCTCTGGATGAACCCACACAGGCATGGATCCCAAGCCCGG	6537
QY	6241	CGGTTCTTGTGGAATGTGCCCTAAGTGTGTTCAAGAGGGGAGATCAGTAGTGCTTACA	6300
Db	6538	CGGTTCTTGTGGAATGTGCCCTAAGTGTGTTCAAGAGGGGAGATCAGTAGTGCTTACA	6597
QY	6301	TCTCATATAGTGAAGAAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6360
Db	6598	TCTCATATAGTGAAGAAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6657
QY	6361	AGGTTTCAGGTGCCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA	6420
Db	6658	AGGTTTCAGGTGCCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACA	6717
QY	6421	ATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGGAAGCCTGTCCAGGATTTCTTTGGA	6480
Db	6718	ATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGGAAGCCTGTCCAGGATTTCTTTGGA	6777
QY	6481	CTTCGATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATACCAAGCTT	6540
Db	6778	CTTCGATTTCTCGGAAGTGTCTTAAAGAGAAACACCGGAACATGCTACAAATACCAAGCTT	6837
QY	6541	CCATCTTCATATCTCTCTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAACGGA	6600
Db	6838	CCATCTTCATATCTCTCTGGCCAGGATATTCAGCATCTCTCCAGAGCAAAAACGGA	6897
QY	6601	CTCCACATAGAAGACTACTCTGTTCTCAGACACACTTCACCAAGTATTTGTGAACCTT	6660
Db	6898	CTCCACATAGAAGACTACTCTGTTCTCAGACACACTTCACCAAGTATTTGTGAACCTT	6957
QY	6661	GCCAAGGACCAAGTGTATGATGACCACTTAAAGACCTCTCATTCACAAAAAACCCAGACA	6720
Db	6958	GCCAAGGACCAAGTGTATGATGACCACTTAAAGACCTCTCATTCACAAAAAACCCAGACA	7017
QY	6721	GTAGTGGACGTTGCAGTTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAGCTAT	6780
Db	7018	GTAGTGGACGTTGCAGTTCACATCTTTTCTACAGGATGAGAAAGTGAAGAAGCTAT	7077
QY	6781	GTAT 6784	
Db	7078	GTAT 7081	
RESULT 14			
AAK51683			
ID	AAK51683	standard; cDNA; 7281 BP.	
XX	AAK51683;		
AC	AAK51683;		
XX			
DT	06-NOV-2001	(first entry)	
XX			
DE	Human polynucleotide SEQ ID NO 228.		
XX			
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorder; arthritis; inflammation; ss.		
XX			
OS	Homo sapiens.		

Db 642 ATTGTGGCTCGCCTGTCTCAGATGCTCGGAGGCTCTCTTTATACAGCCAGAAAGACACC 701
QY 361 AGCATGAAGGACATCGGAAAGTTCTGAGACATTTACAGCAGATCAAGAAATCCAGCTCA 420
Db 702 AGCATGAAGGACATCGGAAAGTTCTGAGACATTTACAGCAGATCAAGAAATCCAGCTCA 761
QY 421 AACTTGAAGCTTCAAGATTTCTGCTGGACAAATGAACCTTCTCTGGGTTCCTATATCAC 480
Db 762 AACTTGAAGCTTCAAGATTTCTGCTGGACAAATGAACCTTCTCTGGGTTCCTGTATCAC 821
QY 481 AACCTCTCTCCAAAGTCTACTGTGACAAAGTCTGAGAGATGCTGAGGCTGTATGTTCCAC 540
Db 822 AACCTCTCTCCAAAGTCTACTGTGACAAAGTCTGAGGCTGTATGTTCCAC 881
QY 541 AAGGTATTTTTCAGAGGTACAGATTACATTTGACAAAGTCTGCAATGGATCAAAATCA 600
Db 882 AAGGTATTTTTCAGAGGTACAGATTACATTTGACAAAGTCTGCAATGGATCAAAATCA 941
QY 601 GAAGAGATGATTTCAACTTTGGTGACCAAGAGTTTCTGAGCTTTTGGCTTACCAAAGGAG 660
Db 942 GAAGAGATGATTTCAACTTTGGTGACCAAGAGTTTCTGAGCTTTTGGCTTACCAAAGGAG 1001
QY 661 AAACCTGGCTGCAGAGAGGAGTACTTGGTCCACATGGACATCCTGAAGCCAAATCTGTG 720
Db 1002 AAACCTGGCTGCAGAGAGGAGTACTTGGTCCACATGGACATCCTGAAGCCAAATCTGTG 1061
QY 721 AGAACACATAAATCTACATCTCCCTCCGAGCAAGGAGCTGGCTGAAGCCCAAAATCA 780
Db 1062 AGAACACATAAATCTACATCTCCCTCCGAGCAAGGAGCTGGCTGAAGCCCAAAATCA 1121
QY 781 TTGCTGCATAGTCTGGGACTCTGCCCAGGAGCTGTTACAGATGAGAGCTGGAGTGAC 840
Db 1122 TTGCTGCATAGTCTGGGACTCTGCCCAGGAGCTGTTACAGATGAGAGCTGGAGTGAC 1181
QY 841 ATGCCACAGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCCTCCACCCAAATC 900
Db 1182 ATGCCACAGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCCTCCACCCAAATC 1241
QY 901 TACAGGCTGTGCTGATGTTCTGCGGGATCCGAGGAGGGGGCTGAAGATCAAG 960
Db 1242 TACAGGCTGTGCTGATGTTCTGCGGGATCCGAGGAGGGGGCTGAAGATCAAG 1301
QY 961 TCTCTCAACTGTATGAGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
Db 1302 TCTCTCAACTGTATGAGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1361
QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAATCTCTTACTGCAATGATTTGATGAAG 1080
Db 1362 GAAGATGCTGAACCTTCTATGACAACTCTACAATCTCTTACTGCAATGATTTGATGAAG 1421
QY 1081 AATTTGAGTCTAGTCTCTCTTCCGCAATATCTGAAAGCTCTGAAGCCGCTGCTCGTT 1140
Db 1422 AATTTGAGTCTAGTCTCTCTTCCGCAATATCTGAAAGCTCTGAAGCCGCTGCTCGTT 1481
QY 1141 GGAAGATCCTGTATACCTGACACTCCAGCCCAAGCCAGGTCATGGCTGAGGTGAAC 1200
Db 1482 GGAAGATCCTGTATACCTGACACTCCAGCCCAAGCCAGGTCATGGCTGAGGTGAAC 1541
QY 1201 AGACCTTCCAGAACTGCTGTGTTCCATGATCTGGAAGGATGTGGAGGAATCTCAGC 1260
Db 1542 AGACCTTCCAGAACTGCTGTGTTCCATGATCTGGAAGGATGTGGAGGAATCTCAGC 1601
QY 1261 CCCAAGATCTGACCTTCTATGAGAAACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTG 1320
Db 1602 CCCAAGATCTGACCTTCTATGAGAAACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTG 1661
QY 1321 GACAGAGGACAAATGACCACTTTTGGGAACAGCAGTGGATGGCTTAGATTTGGACAGCC 1380
Db 1662 GACAGAGGACAAATGACCACTTTTGGGAACAGCAGTGGATGGCTTAGATTTGGACAGCC 1721
QY 1381 CAAGACATGTCGCTTTTGGCAAGCACCAGAGGATGTCAGTCCAGTAAATGTTCT 1440
Db 1722 CAAGACATGTCGCTTTTGGCAAGCACCAGAGGATGTCAGTCCAGTAAATGTTCT 1781

QY 1441 GTGTACACCTGGAGAGCTTTCAACGAGACTAACAGGCAATCCGAGCATATCTCGC 1500
Db 1782 GTGTACACCTGGAGAGAGCTTTCAACGAGACTAACAGGCAATCCGAGCATATCTCGC 1841
QY 1501 TTCTAGAGTGTCTCAACCTGAACAAGCTAGAACCCATAGCAACAGAGTGTGCTCATC 1560
Db 1842 TTCTAGAGTGTCTCAACCTGAACAAGCTAGAACCCATAGCAACAGAGTGTGCTCATC 1901
QY 1561 AACAAAGTCCATGGAGCTGCTGATGAGAGGAGTCTTGGGCTGTATGTTTCACTGGA 1620
Db 1902 AACAAAGTCCATGGAGCTGCTGATGAGAGGAGTCTTGGGCTGTATGTTTCACTGGA 1961
QY 1621 ATTACTCCAGCAGCAATGAGTCCCATCATCTCAAGTACAAGATCCGAATGCAAT 1680
Db 1962 ATTACTCCAGCAGCAATGAGTCCCATCATCTCAAGTACAAGATCCGAATGCAAT 2021
QY 1681 GACAAATGTGAGAGCAAAATAAATCAAGATGGTACTGGGACCCCTGGTCTCGAGCT 1740
Db 2022 GACAAATGTGAGAGCAAAATAAATCAAGATGGTACTGGGACCCCTGGTCTCGAGCT 2081
QY 1741 GACCCCTTTGAGGACATCGGTAGCTCTGCGGGGCTTCGCTACTTGCAGGATGTGGTG 1800
Db 2082 GACCCCTTTGAGGACATCGGTAGCTCTGCGGGGCTTCGCTACTTGCAGGATGTGGTG 2141
QY 1801 GAGCAGGCAATCATCAGGGTCTGACGGGCACCGAGAGAAACTGGTGTCTATATGCAA 1860
Db 2142 GAGCAGGCAATCATCAGGGTCTGACGGGCACCGAGAGAAACTGGTGTCTATATGCAA 2201
QY 1861 CAGATGCCCTATCCCTGTTAGTGTGATGACATCTTCTGCGGGTGTAGAGCCGCTCAATG 1920
Db 2202 CAGATGCCCTATCCCTGTTAGTGTGATGACATCTTCTGCGGGTGTAGAGCCGCTCAATG 2261
QY 1921 CCCCCTTTATGAGCCTGSCCTGGATTTACTCAGTGGTGTGATCATCAAGGGCATCGTG 1980
Db 2262 CCCCCTTTATGAGCCTGSCCTGGATTTACTCAGTGGTGTGATCATCAAGGGCATCGTG 2321
QY 1981 TATGAGAGGAGGACCGCTGAAGAGACCATCGGATCATGGCCCTGGACAAAGCAT 2040
Db 2322 TATGAGAGGAGGACCGCTGAAGAGACCATCGGATCATGGCCCTGGACAAAGCAT 2381
QY 2041 CTCTGGTTTATGCTGTTTCTTATGAGCCTCATCTCTCTTCTTGTGAGCCCTGGCTGCTA 2100
Db 2382 CTCTGGTTTATGCTGTTTCTTATGAGCCTCATCTCTCTTCTTGTGAGCCCTGGCTGCTA 2441
QY 2101 GTGCTCATCTGAGTTAGAAACCTGCTGCCCTACAGTATCCAGGCTGGTGTGTC 2160
Db 2442 GTGCTCATCTGAGTTAGAAACCTGCTGCCCTACAGTATCCAGGCTGGTGTGTC 2501
QY 2161 TTCCCTGCTCGTGTTCCTGCTGAGCAATCCTGAGTCTTCTCTGATTAAGCAGCTCTC 2220
Db 2502 TTCCCTGCTCGTGTTCCTGCTGAGCAATCCTGAGTCTTCTCTGATTAAGCAGCTCTC 2561
QY 2221 TCCAGAGCAACCTGGCAGAGCCCTGGGGGATCATCTACTTACCTGACCTGTACCTGCC 2280
Db 2562 TCCAGAGCAACCTGGCAGAGCCCTGGGGGATCATCTACTTACCTGACCTGTACCTGCC 2621
QY 2281 TACGTCCTGTGTGGCATGGCAGGACTACGTTGGGCTTCACACTCAAGATCTTGCTAGC 2340
Db 2622 TACGTCCTGTGTGGCATGGCAGGACTACGTTGGGCTTCACACTCAAGATCTTGCTAGC 2681
QY 2341 CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTGTGCCCTTTTGGAGAGCAG 2400
Db 2682 CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTGTGCCCTTTTGGAGAGCAG 2741
QY 2401 GGCATTTGAGTCCAGTGGGACAACTGTTGAGAGTCTCTGTGGAGAGATGGCTTCAAT 2460
Db 2742 GGCATTTGAGTCCAGTGGGACAACTGTTGAGAGTCTCTGTGGAGAGATGGCTTCAAT 2801
QY 2461 CTCACACCTTCCATCTCCATGATGCTGTTTGCACCTTCTCTCTATGAGGATGACCTGG 2520
Db 2802 CTCACACCTTCCATCTCCATGATGCTGTTTGCACCTTCTCTCTATGAGGATGACCTGG 2861

QY 2521 TACATTGAGGCTGTCTTTCCAGGCGAGTACGGAAATCCAGGCGCTGGTATTTTCTTTCG 2580
DB 2862 TACATTGAGGCTGTCTTTCCAGGCGAGTACGGAAATCCAGGCGCTGGTATTTTCTTTCG 2921
QY 2581 ACCAAGTCTACTGTTTGGCGAGGAAAGTATGAGAGAGACACCCCTGGTTCACACAG 2640
DB 2922 ACCAAGTCTACTGTTTGGCGAGGAAAGTATGAGAGAGACACCCCTGGTTCACACAG 2981
QY 2641 AAGAGATGTCAGAAATCTGATGAGGAGGAGAACCCACCTTGAAGGTGGCGCTGCC 2700
DB 2982 AAGAGAAATATCAGAAATCTGATGAGGAGGAGAACCCACCTTGAAGGTGGCGCTGCC 3041
QY 2701 ATTCAGAACTGTTAAAGTCTACCGAGATGGATGAAGGTGGCTGTGATGGCGCTGCA 2760
DB 3042 ATTCAGAACTGTTAAAGTCTACCGAGATGGATGAAGGTGGCTGTGATGGCGCTGCA 3101
QY 2761 CTGAATTTTATGAGGCGCAGATCACTCTCTTCCCTGGGCCACAATGGAGCGGGGAGAGC 3161
DB 3102 CTGAATTTTATGAGGCGCAGATCACTCTCTTCCCTGGGCCACAATGGAGCGGGGAGAGC 3161
QY 2821 ACCACATGTCATCTGACCGGGTGTTCCTCCCGCACTCGGGCAACCGCTACATCTG 2880
DB 3162 ACCACATGTCATCTGACCGGGTGTTCCTCCCGCACTCGGGCAACCGCTACATCTG 3221
QY 2881 GGAAGAGCAATTCGGTCTGAGATGAGCACATCCCGGAGAACCTGGGGTCTGTCCCGAG 2940
DB 3222 GGAAGAGCAATTCGGTCTGAGATGAGCACATCCCGGAGAACCTGGGGTCTGTCCCGAG 3281
QY 2941 CATACAGTCTGTTGACATGCTGACTGTGGAAGAACACATCTGTTCTATGCCCGCTG 3000
DB 3282 CATACAGTCTGTTGACATGCTGACTGTGGAAGAACACATCTGTTCTATGCCCGCTG 3341
QY 3001 AAAGGCTCTCTGAGAGCACCTGAAGCGGAGATGGAGCAGATGGCCCTGATGTTGGT 3060
DB 3342 AAAGGCTCTCTGAGAGCACCTGAAGCGGAGATGGAGCAGATGGCCCTGATGTTGGT 3401
QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGAGTGGAAATCAGAGAAAG 3120
DB 3402 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGAGTGGAAATCAGAGAAAG 3461
QY 3121 CTATCTGGCCCTTGGCTTGTGGGGATCTAAGTGTGATCTGATGATGAAACCCACA 3180
DB 3462 CTATCTGGCCCTTGGCTTGTGGGGATCTAAGTGTGATCTGATGATGAAACCCACA 3521
QY 3181 GCTGTGTGGAACCTTACTCCCGCAGGGAATATGGGAGCTGTGCTGAAATACCGACAA 3240
DB 3522 GCTGTGTGGAACCTTACTCCCGCAGGGAATATGGGAGCTGTGCTGAAATACCGACAA 3581
QY 3241 GGCAGCACCATTATCTCTACACACACATGATGAAGCGGAGCTCTGGGGACAGG 3300
DB 3582 GGCAGCACCATTATCTCTCTACACACACATGATGAAGCGGAGCTCTGGGGACAGG 3641
QY 3301 ATTGCGCATCTCCATGGGAAGTGTGCTGTGGGCTCTCTCCCTGTTTCTGAAGAAC 3360
DB 3642 ATTGCGCATCTCCATGGGAAGTGTGCTGTGGGCTCTCTCCCTGTTTCTGAAGAAC 3701
QY 3361 CAGCTGGGAACAGGCTACTACTGCTTGTGTCAGAAAGATGTGGAATCTCCCTCAGT 3420
DB 3702 CAGCTGGGAACAGGCTACTACTGCTTGTGTCAGAAAGATGTGGAATCTCCCTCAGT 3761
QY 3421 TCCTGCAGAAACAGTATGACATGTGTCATACCTGAAAGAGGAGGACAGTGTTCACAG 3480
DB 3762 TCCTGCAGAAACAGTATGACATGTGTCATACCTGAAAGAGGAGGACAGTGTTCACAG 3821
QY 3481 AGCAGTCTGATGCTGGCGCTGGGAGGACCATGAGATGACAGCTGACCATCGATGTC 3540
DB 3822 AGCAGTCTGATGCTGGCGCTGGGAGGACCATGAGATGACAGCTGACCATCGATGTC 3881
QY 3541 TCTGCTATCTCCACCTCATCAGGAAGCATGTGTCGAAGCCCGCTGGTGGAGACATA 3600
DB 3882 TCTGCTATCTCCACCTCATCAGGAAGCATGTGTCGAAGCCCGCTGGTGGAGACATA 3941
QY 3601 GGGCATGAGCTGACCTATGTCTGCCATATGAAGCTGTAGGAGGAGGCGCTTTGTGGAA 3660

DB 3942 GGGCATGAGCTGACCTATGTCTGCCATATGAAGCTGTAAGGAGGAGCCTTTGTGGAA 4001
QY 3661 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGSCATCTCA 3720
DB 4002 CTCCTTCATGAGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGSCATCTCA 4061
QY 3721 GAGACGACCTCTGGAAGAAATATTTCTCAAGGTGGCCCAAGAGAGTGGGTGGATGCTGAG 3780
DB 4062 GAGACGACCTCTGGAAGAAATATTTCTCAAGGTGGCCCAAGAGAGTGGGTGGATGCTGAG 4121
QY 3781 ACCTCAGATGGTACTCTGCCAGCAAGACAGAGCGGGCCCTTCGGGGACACAGCAGC 3840
DB 4122 ACCTCAGATGGTACTCTGCCAGCAAGACAGAGCGGGCCCTTCGGGGACACAGCAGC 4181
QY 3841 TGTCTTCGCCCGTTCACTGAAGATGATGCTGATCCAAATGATTCGACATAGACCCA 3900
DB 4182 TGTCTTCGCCCGTTCACTGAAGATGATGCTGATCCAAATGATTCGACATAGACCCA 4241
QY 3901 GAATCCAGAGACAGACTTGTCTCAGTGGATGGATGGCAAGGGTCTTACCAGGTGAA 3960
DB 4242 GAATCCAGAGACAGACTTGTCTCAGTGGATGGATGGCAAGGGTCTTACCAGGTGAA 4301
QY 3961 GGCTGGAAACTTACACAGCAACAGTGTGGCCCTTTTGGAGAGACTGCTTAATGCC 4020
DB 4302 GGCTGGAAACTTACACAGCAACAGTGTGGCCCTTTTGGAGAGACTGCTTAATGCC 4361
QY 4021 AGCGGAGTCGGAAGGATTTTGTCTCAGATTTGTCTGCCAGCTGTGTTGTCTGCAT 4080
DB 4362 AGCGGAGTCGGAAGGATTTTGTCTCAGATTTGTCTGCCAGCTGTGTTGTCTGCAT 4421
QY 4081 GCCCTTGTCTCAGCCTGATCGTCCACCTTTGGCAAGTACCCAGCTGGAACTTCAG 4140
DB 4422 GCCCTTGTCTCAGCCTGATCGTCCACCTTTGGCAAGTACCCAGCTGGAACTTCAG 4481
QY 4141 CCCTGGATGTACAAACAGACAGTACACATTTGTCCAGCAATGATCTCTGAGGACACGGGA 4200
DB 4482 CCCTGGATGTACAAACAGACAGTACACATTTGTCCAGCAATGATCTCTGAGGACACGGGA 4541
QY 4201 ACCCTGAACTCTTAAGCGCCTTACCAGACCTCGGCTTCGGGACCGCTGTATGGAA 4260
DB 4542 ACCCTGAACTCTTAAGCGCCTTACCAGACCTCGGCTTCGGGACCGCTGTATGGAA 4601
QY 4261 GGAACCCAAATCCAGACACCGCCTGCCAGGAGGAGGAGAGTGGACACTGCCCCA 4320
DB 4602 GGAACCCAAATCCAGACACCGCCTGCCAGGAGGAGGAGAGTGGACACTGCCCCA 4661
QY 4321 GTTCCCGACACCATCATGAGCCTTCTCCAGATGGGAATGGGAATGAGAAACCCCTTCA 4380
DB 4662 GTTCCCGACACCATCATGAGCCTTCTCCAGATGGGAATGGGAATGAGAAACCCCTTCA 4721
QY 4381 CCTGATGTCAGTGTAGCAGCGCAAAATCAAGAAATGCTGCTGTGTGTCGCCAGGG 4440
DB 4722 CCTGATGTCAGTGTAGCAGCGCAAAATCAAGAAATGCTGCTGTGTGTCGCCAGGG 4781
QY 4441 CGAGGGGGTGCCTCCTCCACAAAGAAACAAACACATGAGATATCCTTCAGGACCTG 4500
DB 4782 CGAGGGGGTGCCTCCTCCACAAAGAAACAAACACATGAGATATCCTTCAGGACCTG 4841
QY 4501 ACAGGAAGAAACATTCGGATATCTGGTGAAGACCTATGTGCAGATCATAGCCAAAGC 4560
DB 4842 ACAGGAAGAAACATTCGGATATCTGGTGAAGACCTATGTGCAGATCATAGCCAAAGC 4901
QY 4561 TTAAGAAACAGATCTGGGTGAATGATTTAGTATGGCGGCTTTTCCCTGGGTGTCACT 4620
DB 4902 TTAAGAAACAGATCTGGGTGAATGATTTAGTATGGCGGCTTTTCCCTGGGTGTCACT 4961
QY 4621 AATACTCAAGCACTTCTCCGAGTCAAGAAATTAATGATGCCATCAAAATTAAGAAA 4680
DB 4962 AATACTCAAGCACTTCTCCGAGTCAAGAAATTAATGATGCCATCAAAATTAAGAAA 5021
QY 4681 CACCTAAAGTCGCCAAGACAGTCTTCGAGATCGATTTCTCAACAGCTTGGAAAGATT 4740

Db 5022 CACCTAAAGCTGCCAAGGACAGCTTCTGCAGATCGATTTCCTCAACAGCTTGGGAAGATT 5081
QY 4741 ATGACAGGACTGACACCCAGAAATATATGTCAGGTTGGTTCATATACAAAGGCGCTGGCAT 4800
Db 5082 ATGACAGGACTGACACCCAGAAATATATGTCAGGTTGGTTCATATACAAAGGCGCTGGCAT 5141
QY 4801 GCATCAGCTCTTCTCCTGAATGTCATCAACAATGCCATTCTCCGGGCCCAACCTGCAAAAAG 4860
Db 5142 GCATCAGCTCTTCTCCTGAATGTCATCAACAATGCCATTCTCCGGGCCCAACCTGCAAAAAG 5201
QY 4861 GGAGAGAACCTTAGCATATATGGAATATCTGCTTTCAATCAATCCCTGATCTCAACCAAG 4920
Db 5202 GGAGAGAACCTTAGCATATATGGAATATCTGCTTTCAATCAATCCCTGATCTCAACCAAG 5261
QY 4921 CAGCAGCTCAGAGGTGGCTGTGATGACCAATCAGTGGATGCTCTGTGTCATCTCT 4980
Db 5262 CAGCAGCTCAGAGGTGGCTGTGATGACCAATCAGTGGATGCTCTGTGTCATCTCT 5321
QY 4981 GTCATCTTGTCAATGTCTTGTCCAGGCGAGTTTGTGCTATCTGATCTGATCCAGAGCGG 5040
Db 5322 GTCATCTTGTCAATGTCTTGTCCAGGCGAGTTTGTGCTATCTGATCTGATCCAGAGCGG 5381
QY 5041 GTCAGAAACCAACACCTGCGATGATCAGTGGAGTGAAGCTCTCATCTACTGGCTC 5100
Db 5382 GTCAGAAACCAACACCTGCGATGATCAGTGGAGTGAAGCTCTCATCTACTGGCTC 5441
QY 5101 TCTAATTTTGTCTGGATATGTCAATTTAGTTTGTCTCCCTGCCACACTGGTCAATATCATC 5160
Db 5442 TCTAATTTTGTCTGGATATGTCAATTTAGTTTGTCTCCCTGCCACACTGGTCAATATCATC 5501
QY 5161 TTCTATCTGCTTCCAGAGAGTCTATGTCTGCTCTCCACCAATCTGCTGTAGCCCTT 5220
Db 5502 TTCTATCTGCTTCCAGAGAGTCTATGTCTGCTCTCCACCAATCTGCTGTAGCCCTT 5561
QY 5221 CTACTTTTGTGTATGGTGGTCAATCAGACCTCTCATGTACCAGCCCTCTTGTGTTCTC 5280
Db 5562 CTACTTTTGTGTATGGTGGTCAATCAGACCTCTCATGTACCAGCCCTCTTGTGTTCTC 5621
QY 5281 AGATCCCCAGACAGCTATGTGTTGCTCACCAGGCTGAACCTCTTCAATGGCATTAAT 5340
Db 5622 AGATCCCCAGACAGCTATGTGTTGCTCACCAGGCTGAACCTCTTCAATGGCATTAAT 5681
QY 5341 GGCAGGTGGCCACCTTTGTCTGGAGCTGTTCCACGCAATAAAGCTGAATATATCAAT 5400
Db 5682 GGCAGGTGGCCACCTTTGTCTGGAGCTGTTCCACGCAATAAAGCTGAATATATCAAT 5741
QY 5401 GATATCTGAACTCGTGTCTTGTATCTTCCACATTTTGGCTGGGAGAGGCTCATC 5460
Db 5742 GATATCTGAACTCGTGTCTTGTATCTTCCACATTTTGGCTGGGAGAGGCTCATC 5801
QY 5461 GACATGTGAAAACACAGGCAATGGCTGATGCCCTGSAAGGTTTGGGAGATTCGCTTT 5520
Db 5802 GACATGTGAAAACACAGGCAATGGCTGATGCCCTGSAAGGTTTGGGAGATTCGCTTT 5861
QY 5521 GTGTCAACATTATCTTGGGACTTGGTGGGAGAAACCTCTTCCCATGGCCGTTGAAGG 5580
Db 5862 GTGTCAACATTATCTTGGGACTTGGTGGGAGAAACCTCTTCCCATGGCCGTTGAAGG 5921
QY 5581 GTGGTCTTCTCCTCATTTACTGTCTGATCCAGTACAGATTCTTCATCAGGCCCAACCT 5640
Db 5922 GTGGTCTTCTCCTCATTTACTGTCTGATCCAGTACAGATTCTTCATCAGGCCCAACCT 5981
QY 5641 GTAATGCAAAAGCTATCTCTCTGATGATGAAGATGAAGATGTGAGGGGGGAAAGACAG 5700
Db 5982 GTAATGCAAAAGCTATCTCTCTGATGATGAAGATGAAGATGTGAGGGGGGAAAGACAG 6041
QY 5701 AGAATCTTGATGGTGGAGGCCAGATGACATCTTGAATCAAGGAGTTGACGAAGATA 5760
Db 6042 AGAATCTTGATGGTGGAGGCCAGATGACATCTTGAATCAAGGAGTTGACGAAGATA 6101
QY 5761 TATAGAGGAGGAGGAGCTGCTGTGATGAGGATTTGGTGGGATTCCTCTCTGTGAG 5820
Db 6102 TATAGAGGAGGAGGAGCTGCTGTGATGAGGATTTGGTGGGATTCCTCTCTGTGAG 6161

RESULT 15
ABA09200
ID ABA09200 standard; cDNA; 7086 BP.

QY 5821 TGCCTTGGGCTCCTGGGAGTTAATGGGCTGAAAAATCATCAACTTTCAAGATGTTAACA 5880
Db 6162 TGCCTTGGGCTCCTGGGAGTTAATGGGCTGAAAAATCATCAACTTTCAAGATGTTAACA 6221
QY 5881 GGAGATACCACTGTTTACCAGAGGAGATGCTTCCCTTAACAAAAATAGTATCTTATCAAC 5940
Db 6222 GGAGATACCACTGTTTACCAGAGGAGATGCTTCCCTTAACAAAAATAGTATCTTATCAAC 6281
QY 5941 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6000
Db 6282 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6341
QY 6001 TTGACTGGGAGAGAACACGCTGGAGTTCTTTGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6060
Db 6342 TTGACTGGGAGAGAACACGCTGGAGTTCTTTGCCCTTTTGGAGGAGTCCAGAGAAAGAA 6401
QY 6061 GTTGGCAAGTTGTGTAGTGGGCGATTCGGAACCTGGGCTCGTGAAGTATGGAGAAAA 6120
Db 6402 GTTGGCAAGTTGTGTAGTGGGCGATTCGGAACCTGGGCTCGTGAAGTATGGAGAAAA 6461
QY 6121 TATGCTGTTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
Db 6462 TATGCTGTTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6521
QY 6181 GCGGSCCTCCTGTGTGTCTGGATGAACCCACACAGGATGGATCCCAAAAGCCGG 6240
Db 6522 GCGGSCCTCCTGTGTGTCTGGATGAACCCACACAGGATGGATCCCAAAAGCCGG 6581
QY 6241 CGGTCTTGTGAATGTGCCCTAAGTCTGTCAAGGAGGAGATCAGTAGTCTTACA 6300
Db 6582 CGGTCTTGTGAATGTGCCCTAAGTCTGTCAAGGAGGAGATCAGTAGTCTTACA 6641
QY 6301 TCTCATAGTATGAAGAATGTGAAGCTCTTTGCACTAGATGGCAATCATGTCTCAATGA 6360
Db 6642 TCTCATAGTATGAAGAATGTGAAGCTCTTTGCACTAGATGGCAATCATGTCTCAATGA 6701
QY 6361 AGTTTCAAGTGTGGAGTGTCCAGCATCTAAAAATAGTTTGGAGATGGTTATACA 6420
Db 6702 AGTTTCAAGTGTGGAGTGTCCAGCATCTAAAAATAGTTTGGAGATGGTTATACA 6761
QY 6421 ATAGTTGTACGAATAGCAGGGTCCAAACCCGGACCTGAAGCCCTGTCCAGATTTCTTGA 6480
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QY 6481 CTTGCATTTCTCGAAGTGTCTTAAAGAGAAACCCGGAACATGCTACATACCAGTT 6540
Db 6822 CTTGCATTTCTCGAAGTGTCTTAAAGAGAAACCCGGAACATGCTACATACCAGTT 6881
QY 6541 CCATCTTCAATATCTTCTGCTGCCAGGATATTTCAGCATCTCTCCAGAGCAAAAGGGA 6600
Db 6882 CCATCTTCAATATCTTCTGCTGCCAGGATATTTCAGCATCTCTCCAGAGCAAAAGGGA 6941
QY 6601 CTCCACATAGAAGTACTCTCTTCTTCTCAGCAACACTTGACCAAGTATTTGTGAACCTT 6660
Db 6942 CTCCACATAGAAGTACTCTCTTCTTCTCAGCAACACTTGACCAAGTATTTGTGAACCTT 7001
QY 6661 GCGAGGACCAAGTATGATGACCACTTAAAGAGCTCTCATTACACAAAAACAGACA 6720
Db 7002 GCGAGGACCAAGTATGATGACCACTTAAAGAGCTCTCATTACAAAAACAGACA 7061
QY 6721 GTAGTGGAGTGTGAGTCTCAGATCTTCTACAGGATGAGAAAGTGAAGAAAAAGCTAT 6780
Db 7062 GTAGTGGAGTGTGAGTCTCAGATCTTCTACAGGATGAGAAAGTGAAGAAAAAGCTAT 7121
QY 6781 GTAT 6784
Db 7122 GTAT 7125

XX ABA09200;
 AC
 XX
 XX
 XX 11-JAN-2002 (first entry)
 XX
 XX Human ABCAL homologue-encoding cDNA, SEQ ID NO:976.
 XX
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibitor; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnerary; antiulcer; ss.
 XX
 OS Homo sapiens.
 XX
 XX W0200157188-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 05-FEB-2001; 2001WO-US03800.
 XX
 XX 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 XX
 XX WPI; 2001-457740/49.
 DR P-PSDB; ABB11956.
 DR
 XX
 XX Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 PS Claim 1; Page 833-835; 1963pp; English.
 XX
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides,
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibitor-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a cDNA encoding a
 CC novel human polypeptide of the invention.
 XX
 SQ Sequence 7086 BP; 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
 Query Match 99.7%; Score 6762.2; DB 22; Length 7086;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6770; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 ATGGCTTGTGGCTCAGCTGAGGTGCTGTGGAGAACCTCAGCTTTCAGAGAGA 60
 DB 304 ATGGCTTGTGGCTCAGCTGAGGTGCTGTGGAGAACCTCAGCTTTCAGAGAGA 363
 QY 51 CAACATGTCAGCTGTTACTGGAAGTGGCTGCTATTATTATCTTCCTGATCCTGATC 120
 DB 364 CAACATGTCAGCTGCTGCTGGAAGTGGCTGCTATTATTATCTTCCTGATCCTGATC 423
 QY 121 TCTGTTCGGCTGAGTACCCACCTATGACAAACATGATGCCATTTCGAAATTAAGCC 180
 DB 424 TCTGTTCGGCTGAGTACCCACCTATGACAAACATGATGCCATTTCGAAATTAAGCC 483
 QY 181 ATGCCCTCTGCAGGAACACTTCTTGGGTTGAGGGGATTTCTGTATGCAACAAACCC 240
 DB 484 ATGCCCTCTGCAGGAACACTTCTTGGGTTGAGGGGATTTCTGTATGCAACAAACCC 543
 QY 241 TGTTCCTGTACCGACTCTCTGGGAGGCTCCCGAGGTGTTGGAACACTTACAAATCC 300
 DB 544 TGTTCCTGTACCGACTCTCTGGGAGGCTCCCGAGGTGTTGGAACACTTACAAATCC 603
 QY 301 ATTTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACAC 360
 DB 604 ATTTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACAC 663
 QY 361 AGCATGAAGGACATGCGCAAGTTCTGAGAACATTTACAGCAGATCAAGAATCCAGTCA 420
 DB 664 AGCATGAAGGACATGCGCAAGTTCTGAGAACATTTACAGCAGATCAAGAATCCAGTCA 723
 QY 421 AACTTGAAGCTTCAAGATTTCTCTGTGGACAAATGAACCTTCTCTGGTTCCTATATCAC 480
 DB 724 AACTTGAAGCTTCAAGATTTCTCTGTGGACAAATGAACCTTCTCTGGTTCCTATCAC 783
 QY 481 AACCTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGATTCCTCCAC 540
 DB 784 AACCTCTCTCTCCAAAGTCTACTGTGGACAAAGATGCTGAGGGCTGATGATTCCTCCAC 843
 QY 541 AAGGTATTTTGAAGGCTACAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA 600
 DB 844 AAGGTATTTTGAAGGCTACAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA 903
 QY 601 GAAGAGATGATTAACCTTGGTGACCAAGAGTTTCTGAGCTTTTGTGCCCTACCAAGAGG 660
 DB 904 GAAGAGATGATTAACCTTGGTGACCAAGAGTTTCTGAGCTTTTGTGCCCTACCAAGAGG 963
 QY 661 AAATGCTGTCAGCAGAGGAGTACTTTCGTTTCCAAACATGGACATCTCTGAAGCCAACTCTG 720
 DB 964 AAATGCTGTCAGCAGAGGAGTACTTTCGTTTCCAAACATGGACATCTCTGAAGCCAACTCTG 1023
 QY 721 AGAACAATAACTTACATCTCCCTCCCGAGCAAGGAGCTGGCTGAAGCCACCAAAACA 780
 DB 1024 AGAACAATAACTTACATCTCCCTCCCGAGCAAGGAGCTGGCTGAAGCCACCAAAACA 1083
 QY 781 TTGCTGATAGTCTTGGAGCTCTGGCCAGGAGCTGTTACGATGAGAGCTGGAGTGAC 840
 DB 1084 TTGCTGATAGTCTTGGAGCTCTGGCCAGGAGCTGTTACGATGAGAGCTGGAGTGAC 1143
 QY 841 ATGGACAGGAGGAGTGTATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCAATC 900

Db 1144 ATGCGCAGGAGGTGATGTTCTGACCAATGTGACACCTCCAGCTCCTCCACCCAAATC 1203
QY 901 TACAGGCTGTCTCGTATGTTCTGCGGGGATCCCGAGGAGGGGGCTGAAGATCAAG 960
Db 1204 TACCAGGCTGTCTCGTATGTTCTGCGGGGATCCCGAGGAGGGGGCTGAAGATCAAG 1263
QY 961 TCTCTCAACTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
Db 1264 TCTCTCAACTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1323
QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1080
Db 1324 GAAGATGCTGAACCTTCTATGACAACTCTACAACTCTTACTGCAATGATTTGATGAAG 1383
QY 1081 AATTTGGAGCTAGTCCCTCTTCCCGCATATCTGGAAGCTCTGGAAGCCCTGCTCGTT 1140
Db 1384 AATTTGGAGCTAGTCCCTCTTCCCGCATATCTGGAAGCTCTGGAAGCCCTGCTCGTT 1443
QY 1141 GGAAGATCTCTATACACCTTGACACTCCAGCCACAAGCAGGTCATGGCTGAGGTGAAC 1200
Db 1444 GGAAGATCTCTATACACCTTGACACTCCAGCCACAAGCAGGTCATGGCTGAGGTGAAC 1503
QY 1201 AGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGCATGTGGAGGAACCTCAGC 1260
Db 1504 AGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGCATGTGGAGGAACCTCAGC 1563
QY 1261 CCCAAGATCTGACCTTCTGATGAGAACAGCCCAAGAAATGGACCTTGTCCGGATGCTGTG 1320
Db 1564 CCCAAGATCTGACCTTCTGATGAGAACAGCCCAAGAAATGGACCTTGTCCGGATGCTGTG 1623
QY 1321 GACAGCAGGACAATGACCACTTTGGGAACAGCAGTGTGGATGGCTAGATTTGGACAGCC 1380
Db 1624 GACAGCAGGACAATGACCACTTTGGGAACAGCAGTGTGGATGGCTAGATTTGGACAGCC 1683
QY 1381 CAAGACATCGTGGCTTTTGGCCAAAGCACCAGAGGATGTCAGCTCCAGTAATGGTTCT 1440
Db 1684 CAAGACATCGTGGCTTTTGGCCAAAGCACCAGAGGATGTCAGCTCCAGTAATGGTTCT 1743
QY 1441 GTGTACCTGGAGAGAGCTTTCAACGAGACTAACAGGCAATCCGAGCAATATCTCGC 1500
Db 1744 GTGTACCTGGAGAGAGCTTTCAACGAGACTAACAGGCAATCCGAGCAATATCTCGC 1803
QY 1501 TTCAATGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1560
Db 1804 TTCAATGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1863
QY 1561 AACAAATCCATGGAGTGTGATGAGAGGAAATTTCTGGGCTGTTATTTGTTCACTGGA 1620
Db 1864 AACAAATCCATGGAGTGTGATGAGAGGAAATTTCTGGGCTGTTATTTGTTCACTGGA 1923
QY 1621 ATTACTCCAGGAGGATGAGTGTGCTGCTCCCATCATGTCAAGTACAAAGATCGGATGACAT 1680
Db 1924 ATTACTCCAGGAGGATGAGTGTGCTGCTCCCATCATGTCAAGTACAAAGATCGGATGACAT 1983
QY 1681 GACAATGTGGAGGACAAATAAATAAAGGATGGGTACTGGGACCCCTGGTCTCGAGCT 1740
Db 1984 GACAATGTGGAGGACAAATAAATAAAGGATGGGTACTGGGACCCCTGGTCTCGAGCT 2043
QY 1741 GACCCCTTTGAGGAGATGGGTGATGCTGCGGGGGCTTCGCTACTTTCGAGGATGTTG 1800
Db 2044 GACCCCTTTGAGGAGATGGGTGATGCTGCGGGGGCTTCGCTACTTTCGAGGATGTTG 2103
QY 1801 GAGCAGGCAATCATCAGGCTGTGACGGGACCCGAGAGAAACTGGTCTATATGAA 1860
Db 2104 GAGCAGGCAATCATCAGGCTGTGACGGGACCCGAGAGAAACTGGTCTATATGAA 2163
QY 1861 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTCGGGGTGATGAGCCGGTCAATG 1920
Db 2164 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTCGGGGTGATGAGCCGGTCAATG 2223
QY 1921 CCCCTCTCATACGCTGCCCTGGATTTACTACGTGGCTGTGATCATCAAGGGCATCGT 1980

Db 2224 CCCCTCTCATGACGCTGGCTGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 2283
QY 1981 TATGAGAGGAGGACCGCTGAAAGAGACCATCGGGATCATGGCCCTGGACACAGCAT 2040
Db 2284 TATGAGAGGAGGACCGCTGAAAGAGACCATCGGGATCATGGCCCTGGACACAGCAT 2343
QY 2041 CTCTGGTTTACGTGGTTCATTTAGTAGCTCATCTCTCTTCTTGAGCGCTGGCTGCTA 2100
Db 2344 CTCTGGTTTACGTGGTTCATTTAGTAGCTCATCTCTCTTCTTGAGCGCTGGCTGCTA 2403
QY 2101 GTGTCTATCTGAAAGTTAGGAAACCTGCTGCCCTACAGTATCCAGCGGTGGTGTTC 2160
Db 2404 GTGTCTATCTGAAAGTTAGGAAACCTGCTGCCCTACAGTATCCAGCGGTGGTGTTC 2463
QY 2161 TTCTGTCCGCTGTTGCTGTGGTGACAACTCTGCGAGTCTTCCGATTAGCACACTCTC 2220
Db 2464 TTCTGTCCGCTGTTGCTGTGGTGACAACTCTGCGAGTCTTCCGATTAGCACACTCTC 2523
QY 2221 TCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATCTACTTTCACGCTGTACCTGCC 2280
Db 2524 TCCAGAGCCAACTGGCAGCAGCCTGTGGGGCATCATCTACTTTCACGCTGTACCTGCC 2583
QY 2281 TACCTCTGTGTGGCATGSCAGSACTAGTGGGCTTCACACTCAAGATCTTCGCTAGC 2340
Db 2584 TACCTCTGTGTGGCATGSCAGSACTAGTGGGCTTCACACTCAAGATCTTCGCTAGC 2643
QY 2341 CTGCTGTCTCCTGTGGCTTTTGGTGTGGTGTGAGTACTTTCGCCCTTTTGGAGGACG 2400
Db 2644 CTGCTGTCTCCTGTGGCTTTTGGTGTGGTGTGAGTACTTTCGCCCTTTTGGAGGACG 2703
QY 2401 GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTCTGTGGAGAGAGTGGCTTCAAT 2460
Db 2704 GGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTCTGTGGAGAGAGTGGCTTCAAT 2763
QY 2461 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGTGATGACCTGG 2520
Db 2764 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGTGATGACCTGG 2823
QY 2521 TACATTGAGGCTGTCTTTCAGGCGCAGTACCGAATTCAGGCGCCTGGTATTTCCCTTGC 2580
Db 2824 TACATTGAGGCTGTCTTTCAGGCGCAGTACCGAATTCAGGCGCCTGGTATTTCCCTTGC 2883
QY 2581 ACCAAGTCTACTGTTTGGCGAGGAAAGTATGAGAGAGCCACCTGGTTCACCAACGAG 2640
Db 2884 ACCAAGTCTACTGTTTGGCGAGGAAAGTATGAGAGAGCCACCTGGTTCACCAACGAG 2943
QY 2641 AAGAGATGTGAGAAATCTGATGGAGAGAACCCACCCACTTTGAAGCTGGGCGTGTCC 2700
Db 2944 AAGAGATGTGAGAAATCTGATGGAGAGAACCCACCCACTTTGAAGCTGGGCGTGTCC 3003
QY 2701 ATTGAGAACCTGTAAAGTCTACCGAGATGGATGAGGTGGCTGTGCGATGGCTGGCA 2760
Db 3004 ATTGAGAACCTGTAAAGTCTACCGAGATGGATGAGGTGGCTGTGCGATGGCTGGCA 3063
QY 2761 CTGAATTTTATGAGGCGCAGATCACCTCTCTTCTGGGCCAATGGAGCGGGGAAGACG 2820
Db 3064 CTGAATTTTATGAGGCGCAGATCACCTCTCTTCTGGGCCAATGGAGCGGGGAAGACG 3123
QY 2821 ACCACCATGTCAATCTGACCGGGTGTTCCTCCCGACCTCGGCGACCGCTACATCTG 2880
Db 3124 ACCACCATGTCAATCTGACCGGGTGTTCCTCCCGACCTCGGCGACCGCTACATCTG 3183
QY 2881 GGAAAAGACATTCGCTGTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCGAG 2940
Db 3184 GGAAAAGACATTCGCTGTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCGAG 3243
QY 2941 CATACGTGCTGTTGATGCTGACTGTGGAAGAACATCTGGTCTGATGCGCGGTG 3000
Db 3244 CATACGTGCTGTTGATGCTGACTGTGGAAGAACATCTGGTCTGATGCGCGGTG 3303
QY 3001 AAAGGCTCTCTGAGAGCAGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3060
Db 3304 AAAGGCTCTCTGAGAGCAGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3363

QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAAAGCCAGCTGTCTAGGTGGAATGAGAGAAAG 3120
DB 3364 TTGCCATCAAGCAAGCTGAAAGCAAAACAAAGCCAGCTGTCTAGGTGGAATGAGAGAAAG 3423
QY 3121 CTATCTGTGGCCCTTGGCCCTTTGCGGGGATCTAAGGTGTGATCTCTGATGAAACCCACA 3180
DB 3424 CTATCTGTGGCCCTTGGCCCTTTGCGGGGATCTAAGGTGTGATCTCTGATGAAACCCACA 3483
QY 3181 GCTGTGTGGACCCCTTACTTCCCGCAGGGGAATATGGGAGCTGTCTCTGAAATACCGACAA 3240
DB 3484 GCTGTGTGGACCCCTTACTTCCCGCAGGGGAATATGGGAGCTGTCTCTGAAATACCGACAA 3543
QY 3241 GCGCGACCATTAATCTCTCTACACACACATGATGAAGGGAGCGTCTCTGGGGACAGG 3300
DB 3544 GCGCGACCATTAATCTCTCTACACACACATGATGAAGGGAGCGTCTCTGGGGACAGG 3603
QY 3301 ATTGCCATCATCTCCATGGGAGCTGTCTGTGTGGCTCTCTCCCTGTCTTCTGAAGAAC 3360
DB 3604 ATTGCCATCATCTCCATGGGAGCTGTCTGTGTGGCTCTCTCCCTGTCTTCTGAAGAAC 3663
QY 3361 CAGCTGGGAACAGGCTACTACCTTGGTTCAGAAAGATGTGGAATCTCTCCCTCAGT 3420
DB 3664 CAGCTGGGAACAGGCTACTACCTTGGTTCAGAAAGATGTGGAATCTCTCCCTCAGT 3723
QY 3421 TCTTCGAGAACAGTAGTACCTGTCTACCTGAAAGAGGAGGACAGTGTCTCAG 3480
DB 3724 TCTTCGAGAACAGTAGTACCTGTCTACCTGAAAGAGGAGGACAGTGTCTCAG 3783
QY 3481 AGCAGTTCTGATCTGGCTGGGACGACCATGAGAGTGACACGCTGACCATCGATGTC 3540
DB 3784 AGCAGTTCTGATCTGGCTGGGACGACCATGAGAGTGACACGCTGACCATCGATGTC 3843
QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTCTGAAGCCCGGCTGGTGGAGACATA 3600
DB 3844 TCTGCTATCTCCAACTCATCAGGAAGCATGTCTGAAGCCCGGCTGGTGGAGACATA 3903
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DB 3904 GGGCATGAGCTGACCTATGTCTGCTCAATGATGAAGCTGCTAAGGAGGAGCCCTTTGTGAA 3963
QY 3661 CTCCTTCATGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 3720
DB 3964 CTCCTTCATGATGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCA 4023
QY 3721 GAGAGACCCCTGGAGAAATATTTCTCAAGGTGGCCGAGAGAGTGGGTGGATGCTGAG 3780
DB 4024 GAGAGACCCCTGGAGAAATATTTCTCAAGGTGGCCGAGAGAGTGGGTGGATGCTGAG 4083
QY 3781 ACCTCAGATGTTACCTTCCGACGACGAGCAAGAGCGGGGCTTCGGGACACGACAGC 3840
DB 4084 ACCTCAGATGTTACCTTCCGACGACGAGCAAGAGCGGGGCTTCGGGACACGACAGC 4143
QY 3841 TGTCTTCCCGCTTCACTGAAGATGATGCTGTATCCAAATGATTTCTGACATAGACCCA 3900
DB 4144 TGTCTTCCCGCTTCACTGAAGATGATGCTGTATCCAAATGATTTCTGACATAGACCCA 4203
QY 3901 GAATCCGAGAGACAGACTTCTCAGTGGGATGATGGCAAGAGGTCTACCGAGTAAA 3960
DB 4204 GAATCCGAGAGACAGACTTCTCAGTGGGATGATGGCAAGAGGTCTACCGAGTAAA 4263
QY 3961 GCGTGAACCTTACACGACAGCTTGTGGCCCTTTTGTGGAGAGACTGCTAATGGCC 4020
DB 4264 GCGTGAACCTTACACGACAGCTTGTGGCCCTTTTGTGGAGAGACTGCTAATGGCC 4323
QY 4021 AGCGGAGTCGGAAGGATTTTGTCTCAGATTTCTTGGCAGCTGTGTGTCTGCAAT 4080
DB 4324 AGCGGAGTCGGAAGGATTTTGTCTCAGATTTCTTGGCAGCTGTGTGTCTGCAAT 4383
QY 4081 GCGCTGTGTTACGCTGATCGTCCACCCCTTGGCAAGTACCCAGCTGGAACTTCAG 4140
DB 4384 GCGCTGTGTTACGCTGATCGTCCACCCCTTGGCAAGTACCCAGCTGGAACTTCAG 4443

QY 4141 CCCTGGATGTAAACGAACAGTACACATTTGTCTAGCAATGATGCTCTGAGGACACGGGA 4200
DB 4444 CCCTGGATGTAAACGAACAGTACACATTTGTCTAGCAATGATGCTCTGAGGACACGGGA 4503
QY 4201 ACCCTGGAACCTTTAAAGCCCTTACCAAGACCCCTGGCTTCGGGAGCCCTCTATGGAA 4260
DB 4504 ACCCTGGAACCTTTAAAGCCCTTACCAAGACCCCTGGCTTCGGGAGCCCTCTATGGAA 4563
QY 4261 GGAACCCCAATCCAGACACGCCCTGCCAGGAGGAGAGAGTGAGCCACTGCCCA 4320
DB 4564 GGAACCCCAATCCAGACACGCCCTGCCAGGAGGAGAGAGTGAGCCACTGCCCA 4623
QY 4321 GTTCCCGACACATCATGAGCCCTTCCGAATGGGAACCTGGAATGCAAGAACCCCTTCA 4380
DB 4624 GTTCCCGACACATCATGAGCCCTTCCGAATGGGAACCTGGAATGCAAGAACCCCTTCA 4683
QY 4381 CCTGCATGCCAGTGTAGCAGCAGCAAAATCAAGAAGATGCTGCTGTGTGTCGCCAGG 4440
DB 4684 CCTGCATGCCAGTGTAGCAGCAGCAAAATCAAGAAGATGCTGCTGTGTGTCGCCAGG 4743
QY 4441 GCAGGGGGCTGCTCTCTCCACAAAGAAACAAACACTGCAGATATCTTTCAGGACCTG 4500
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DB 4984 CACCTAAGCTGGCAGGACAGTCTGCGAGATCGATTTCTCAACAGCTTGGGAAGATT 5043
QY 4741 ATGACAGGATGACACAGCAAAATATGTCAGAGTGTGGTTCAATAACAGGCGTGGCAT 4800
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DB 5104 GCAATCAGCTCTTCTGATGTATCAACAATGCCATTTCTCGGGCCCAACCTGCAAAAG 5163
QY 4861 GGAGAGAACCCCTAGCCATTAATGGAATTAATGCTTTCAATCATCCCTGAATCTACCAAG 4920
DB 5164 GGAGAGAACCCCTAGCCATTAATGGAATTAATGCTTTCAATCATCCCTGAATCTACCAAG 5223
QY 4921 CAGCAGCTCTCAGAGTGGCTCTGATGACACATCAGTGTGATGCTGTGTGTCATCTCT 4980
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QY 4981 GTCATCTTTGCAATGTCCTTCCAGCCAGCTTTGTCGTATTTCTGATTCAGGAGCGG 5040
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QY 5041 GTCAGAAACCAACACCTGCAAGTTCATCAGTGGAGTGAAGCTGTCTACTTGGCTC 5100
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QY 5101 TCTAATTTTCTCTGGGATATGTCATTAATGCTTCCCTGCCACACTGCTCATATCATC 5160
DB 5404 TCTAATTTTCTCTGGGATATGTCATTAATGCTTCCCTGCCACACTGCTCATATCATC 5463
QY 5161 TTTCTGCTTCCAGCAGAGTCTTATGTCCTCCACCAATCTGCTGTGTGTAGCCCTT 5220
DB 5464 TTTCTGCTTCCAGCAGAGTCTTATGTCCTCCACCAATCTGCTGTGTGTAGCCCTT 5523
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QY |||||||
5281 AAGATCCCGACACACCTTATGTGTGCTCACACGGTGAACCTCTTCAATGGCAATTAAT 5340
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QY |||||||
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QY |||||||
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QY |||||||
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Db |||||||
6004 AGAATCTTGATGGTGGAGCCAGATGACATCTTGAATCAAGGAGTTGACGAGATA 6063
QY |||||||
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QY |||||||
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QY |||||||
5881 GGAGATACCACTGTTACAGAGGAGATGCTTTCCTTAAACAAAATAGTATCTTATCAAC 5940
Db |||||||
6184 GGAGATACCACTGTTACAGAGGAGATGCTTTCCTTAAACAAAATAGTATCTTATCAAC 6243
QY |||||||
5941 ATCCATGAAGTACATCAGAACATGGGCTACTGCCCCTCAGTTTGTATGCCATCACAGAGCTG 6000
Db |||||||
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QY |||||||
6001 TTGACTGGGAGAGAACACAGTGGAGTTCTTTGGCCCTTTTGGAGGAGTCCCGACAGAAAGAA 6060
Db |||||||
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QY |||||||
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Db |||||||
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QY |||||||
6121 TATGCTGGTAACTATAGTGGAGGCAACAGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
Db |||||||
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QY |||||||
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Db |||||||
6484 GCGGGGCTCCTGTGGTGTTCCTGGATGAACCCACACAGGATGGATCCCAAGGCCCG 6543
QY |||||||
6241 CGGTTCTTGTGGAATTTGTGCCCTTAAGTGTGTCAAGGAGGAGATCAGTAGTGTAC 6300
Db |||||||
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QY |||||||
6301 TCTCATAGTATGAAGATGTGAAGCTCTTTGCACTAGATGGCAATCATGGTCAATGGA 6360
Db |||||||

Db 6604 TCTCATAGTATGAAGATGTGAAGCTCTTTGCATAGGATGGCAATCATGGTCAATGGA 6663
QY |||||||
6361 AGGTTTCAGTGCCTTGGCAGTGTCCAGCATCTAAAAATAGTTTGGAGATGGTTATACA 6420
Db |||||||
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QY |||||||
6421 ATAGTTGTACGAATAGCAGGTTCCAAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6480
Db |||||||
6724 ATAGTTGTACGAATAGCAGGTTCCAAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGA 6783
QY |||||||
6481 CTTGCAATTTCTGGAGTGTCTTAAAGAGAAACACCGGACATGCTTACAATACCACTT 6540
Db |||||||
6784 CTTGCAATTTCTGGAGTGTCTTAAAGAGAAACACCGGACATGCTTACAATACCACTT 6843
QY |||||||
6541 CCATCTTTCATTTCTCTGCCCAGGATATTTCAGCATCTCTCCAGAGCAAAAAGCGA 6600
Db |||||||
6844 CCATCTTTCATTTCTCTGCCCAGGATATTTCAGCATCTCTCCAGAGCAAAAAGCGA 6903
QY |||||||
6601 CTCCACATAGAGACTACTCTGTTTCTCAGACACACTTGGACCAAGTATTTGTGAACCTT 6660
Db |||||||
6904 CTCCACATAGAGACTACTCTGTTTCTCAGACACACTTGGACCAAGTATTTGTGAACCTT 6963
QY |||||||
6661 GCACAGGACCAAGTGTGATGACCACTTAAAGACCTCTCATTTACACAAAACCCAGACA 6720
Db |||||||
6964 GCACAGGACCAAGTGTGATGACCACTTAAAGACCTCTCATTTACACAAAACCCAGACA 7023
QY |||||||
6721 GTAGTGGAGCTTGTGAGTGTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
Db |||||||
7024 GTAGTGGAGCTTGTGAGTGTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 7083
QY |||||
6781 GTA 6783
Db 7084 GTA 7086

Search completed: April 3, 2003, 13:43:17
Job time : 1223.47 secs

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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 186.553 Seconds
(without alignments)
11152.306 Million cell updates/sec

Title: US-09-595-526C-1_COPY_291_7074
Perfect score: 6784
Sequence: 1 atggctttgttgctcgaact.....agtgaaagaagctatgtat 6784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 892724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	430.8	6.4	5894	3	US-08-665-259-24
2	430.8	6.4	5894	3	US-08-762-500-24
3	430.8	6.4	6525	3	US-08-762-500-74
4	56	0.8	7218	1	US-08-232-463-14
5	54.4	0.8	6846	4	US-08-961-527-198
6	52.4	0.8	2726	1	US-08-461-823-1
7	52.4	0.8	4646	1	US-08-181-471-2
8	52.4	0.8	4669	2	US-08-583-276-18
9	52.4	0.8	4669	6	5206352-3
10	52.4	0.8	6505	2	US-08-793-610-5
11	52.4	0.8	9318	2	US-08-793-610-6
12	52.4	0.8	4403765	4	US-09-103-840A-2
13	52.4	0.8	4411529	4	US-09-103-840A-1
14	51.6	0.8	729	4	US-09-134-001C-995
15	51.4	0.8	2381	4	US-09-221-017B-812
16	50.8	0.7	4264	2	US-08-784-649A-1
17	50.8	0.7	4264	2	US-08-784-649A-5
18	50.2	0.7	6273	4	US-08-961-527-21
19	50	0.7	6854	4	US-09-194-905-7
20	49.4	0.7	4233	3	US-09-120-513-1
21	49.4	0.7	4233	4	US-09-450-105-1
22	49.2	0.7	775	4	US-08-961-527-264
23	49.2	0.7	4669	2	US-08-752-447-1
24	49.2	0.7	4669	4	US-09-316-167-1
25	49.2	0.7	7174	4	US-08-961-527-189
26	49	0.7	5045	4	US-09-390-721-1
27	49	0.7	5045	4	US-09-390-721-3

c	28	46.2	0.7	7218	1	US-08-232-463-14	Sequence 14, Appl
	29	45.2	0.7	23673	4	US-09-773-816-1	Sequence 1, Appl
c	30	44.2	0.7	1526	4	US-08-858-207A-34	Sequence 34, Appl
	31	44.2	0.7	12127	4	US-08-961-527-148	Sequence 148, Appl
	32	43	0.6	15567	4	US-09-627-376-3	Sequence 3, Appl
	33	42.4	0.6	1518	2	US-08-997-080-88	Sequence 88, Appl
	34	42.4	0.6	1518	2	US-08-997-362-88	Sequence 88, Appl
	35	42.4	0.6	1518	3	US-08-873-970-88	Sequence 88, Appl
	36	42.4	0.6	1518	4	US-09-095-855-88	Sequence 88, Appl
	37	42.4	0.6	1518	4	US-09-324-542-88	Sequence 88, Appl
	38	42.4	0.6	1518	4	US-09-205-426-88	Sequence 88, Appl
	39	42.2	0.6	933	4	US-09-134-001C-2350	Sequence 2350, Ap
	40	42	0.6	5717	4	US-08-961-527-102	Sequence 102, Ap
	41	41.2	0.6	900	4	US-09-134-001C-1330	Sequence 1330, Ap
c	42	41	0.6	25002	4	US-08-961-527-48	Sequence 48, Appl
	43	40.8	0.6	1971	4	US-08-838-207A-72	Sequence 72, Appl
	44	40	0.6	648	4	US-09-305-984-17	Sequence 17, Appl
	45	40	0.6	648	4	US-09-073-541A-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-665-259-24
; Sequence 24, Application us/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES.
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG5-9.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..5053
US-08-665-259-24

Query Match 6.4%; Score 430.8; DB 3; Length 5894;

[illegible]

RESULT 2
 US-08-762-500-24
 ; Sequence 24, Application US/08762500
 ; Patent No. 6030806
 ; GENERAL INFORMATION:
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Burn, Timothy C.
 ; APPLICANT: Connors, Timothy D.
 ; APPLICANT: Dackowski, William R.
 ; APPLICANT: van Raay, Terence J.
 ; APPLICANT: Klinger, Katherine W.
 ; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
 ; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
 ; NUMBER OF SEQUENCES: 83
 ; CORRESPONDENCE ADDRESS:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/762,500
FILING DATE: 09-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10469
FILING DATE: 17-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG5-9.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 5894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 2..5053
US-08-762-500-24

Query Match 6.4%; Score 430.8; DB 3; Length 5894;
Best Local Similarity 56.1%; Pred. No. 4,1e-122;
Matches 944; Conservative 0; Mismatches 692; Indels 48; Gaps 5;

QY 1760 GGTACGCTGGGGGGCTTCGCTACTTCAGAGATGGTGGAGCAGGGAATCATCAGGG 1819
DB 555 GGTACATCGGGGAAGGCTTCCTGGCGGTGAGCATCTGGACGGCGGCATCGAGT 614
QY 1820 TGTGACGGGACCGGAGA-----AGAAACTGGTGCTATATGCAACAGA 1864
DB 615 ACCATGCCGATGCCGCCACAGCCAGCTGTTCCAGAGACTGACGGTGACCATCAGAGT 674
QY 1865 TGCCCTATCCCTGTTACGTTGATGACATCTTTCTGGGGTGTAGACCGGTCAATGCCCC 1924
DB 675 TCCCGTACCGCGGTTTCATCGGAGACCCCTTCTCGTGCCCATCCAGTACCAGCTGCCCC 734
QY 1925 TCTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGCGATCGTGATG 1984
DB 735 TGTGCTGTGCTTCAGCTTCACCTACACCGCGCTCACCATTGCCGCTGCTGTGTCGACGG 794
QY 1985 AGAAGGAGGACCGCTGAAAGAGACCATCGGATCATGGGCTGGACAAACAGCATACTCT 2044
DB 795 AGAAGAAAGGAGGCTGAAGGAGTACATGGCATGATGGGCTCAGCAGCTGCTGCACT 854
QY 2045 GGTTCAGCTGGTTCATTAGTACCTCATTCCTTCTTGTGAGCGCTGGCCTGCTAGTGG 2104
DB 855 GGAGTGGCTGGTTCCTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 914
QY 2105 TCATCTCTGAAGTTA-----GGAAACCTGCTGCCCTACAGTATCCACGG 2149
DB 915 TGCTCTCTGTCAGGTGAAGCAAAATGTAGCCGCTGCTGCCCGCAGGACCCCTCCC 974
QY 2150 TGTGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2209
DB 975 TGTGTCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1034
QY 2210 GCACACTCTTCTCCAGAGCAACCTGGAGAGCGCTGTGGGGCATCATCTACTTCCACGC 2269
DB 1035 GCACCTTCTTCCAGAAAGCAACATGGAGAGCCCTTCGAGGCTTCTTCTTCTTCTTCTTCT 1094
QY 2270 TGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGACTACGTTGGGCTTTCACACTCAAGA 2329
DB 1095 CCTACATCCCTACTTCTTCTGTTGGGCCCCCTGGGTACAACTGGATGACTCTGAGCCAGAAGC 1154

QY 2330 TCTTCGCTAGCCTGCT 2389
DB 1155 TCTGCT 1214
QY 2390 TTGAGGACAGGGCAATGGAGTGCAGTGGGACACACCTCTTTTGGAGTCTCTCTCTCTCTCT 2449
DB 1215 TTGAGCGAAAGGCATGGGCATCCAGTGGCGAGACCTCTCTGAGTCCCTCAACCTGGACG 1274
QY 2450 ATGGCTTCAATCTCTACCACTTCGATCTCCATGATCTCTTTTGACACCTTCTCTCTATGGG 2509
DB 1275 ACGACTTCT 1334
QY 2510 TGATGACCTGTGTACATTCAGGCTGTCTTTTCCAGGCCATACGGAATTCCTCAGGCGCTGGT 2569
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QY 2570 ATTTTCTCTTGACCAAGTCTACTGTTTGGGAGGAAAGTATG-----AGAGA 2620
DB 1395 ACTTCTTCT 1454
QY 2621 GCCACCTGGTTCCAAACGAGAGAAATGTTCAGAAATTCGATGGAGGAGAAACCCACCC 2680
DB 1455 AAGAAGACAGTACCCCGAGAAAGCACTCAGAAACAGTACTTTGAAGCCGAGCCAGAGG 1514
QY 2681 ACTTGAAGCTGGCGGTGTCCTTTCAGAACCTGGTAAAGTCTACCGAGATGGATGA-- 2738
DB 1515 ACCTGCTGGCGGGATCAAGATCAAGCACCTGTCCAGGGTGTTCAGGGTGGGAAATAAG 1574
QY 2739 -----GGTGGCTGTGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACTCTCTTCC 2794
DB 1575 ACAGGGCGGCGCTCAGAGACCTGAACCTCAACCTGTACGAGGACAGATACCCGCTCTGC 1634
QY 2795 TGGGCCCAATGGAGCGGGGAGAGACGACCACTCAATCTGACCGGGTGTTCCTCCC 2854
DB 1635 TGGGCCCAACAGGTGCGGGGAGAGACCACTCAATCTGACCGGGTGTTCCTCCC 1694
QY 2855 GCACTCTGGGACACCGCTTACCTTGGGAAAGACATTCGCTCTCAGATGAGCACCATCC 2914
DB 1695 CCACAGTGGAGCGGCATACATCAGCGGTATGAATTTCCAGGACATGTTTCAGATCC 1754
QY 2915 GGCAGAACTGGGGCTGTGTCCTCCAGCATACGTCGCTTTTGACATGCTGACTGTCGAAG 2974
DB 1755 GGAAGAGCTGGGCTGTGTCCTCCAGCATACCTCTGTTGACAACTTGACAGTCCGAG 1814
QY 2975 AACACATCTGTTCTATGCCGCTTGAAGGGCTCTCTGAGNAGCACCTGAGGCGGAGA 3034
DB 1815 AGCACTTTATTTTACGCCAGCTGAGGGCTGTACGTCAGAGTGGCTTGAAGAG 1874
QY 3035 TGGAGCAGATGGCCTGGATGTTGTTTGGCATCAAGCAAGCTGAAAGCAAAACAAGCC 3094
DB 1875 TCAAGCAGATG---CTGCACATCATCGCCTGGAGGACAAAGTGAACCTACGAGGCGCT 1931
QY 3095 AGCTGTCAGGTGAATGACAGAAAGCTATCTGTGGCTTGGCCTTTGCGGGGATCTA 3154
DB 1932 TCCTGAGCGGGGCGATGAGGCGCAAGCTCTCCATCGGATCGCCTCATCGAGGCTCCA 1991
QY 3155 AGTGTGTCATTTCTGATGAACCCAGCTGTGTGGACCTTACTCCCGCAGGGGAATAT 3214
DB 1992 AGGTGCTGATCTGAGCAGGCCACCTCGGGCATGGACGCTATCCAGGAGGCGCATCT 2051
QY 3215 GGGAGCTGCTGTAATACCGAAGCGCCGACCATTTATCTCTCTACACACACATGG 3274
DB 2052 GGGATCTTCTTTCAGCGGAGAAAGTACCGCACCATCTGCTGACCAACCCACTTCATGG 2111
QY 3275 ATGAAGCGGACGCTCTCTGGGGGACAGGATTCCTCATCTCCCATGGGAGCTGTCTGTG 3334
DB 2112 ACGAGGCTGACCTGCTGGGAGACCGCATCGCCATCATGCCAAGGGGAGCTGCACTGCT 2171
QY 3335 TGGGCTCTCTCTCTTCTTGAAGAACCGAGCTGGGAAACAGGCTACTACCTGAGCTTGGTCA 3394
DB 2172 GGGGCTCTCTCTCTTCTTCAAGCAGAAATACGGTGGCGGTATCACATGAGCTGGTGA 2231
QY 3395 AGAA 3398

REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
LENGTH: 6846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-198

Query Match 0.8%; Score 54.4; DB 4; Length 6846;
Best Local Similarity 54.6%; Pred. No. 1.8e-05;
Matches 131; Conservative 0; Mismatches 106; Indels 3; Gaps 1;

QY 3098 TGTGAGTGAATGCAGAGAAAGCTATCTGTGGCCCTTGGCCCTTGTGGGGGGATCTAAGG 3157
DB 4805 TGTGAGCGGGCAAAAGCTCTCTCTCTTTTGTCTTGTACCTTGATTGGCGACCAAGC 4746
QY 3158 TTGTCATTCTGGATGAACCCACAGCTGGTGTGGACCCCTTACTCCCGCAGGGGAATATGG 3217
DB 4745 TTGTCCTTTTAGATGAACCAACTGCTGCCATGGATCTTCAACTCGTCAACGCTTTTGGG 4686
QY 3218 AGCTGTGTGTGA---ATACCGACAAGCGCGCACCACTTATCTCTACACACCATGG 3274
DB 4685 AATCGTTCGGGACCTAAAGCCAGGACTACGATTCTCTATCTCTCTCTATATATG 4626
QY 3275 ATGAAGGAGCTGCTGGGGACAGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTG 3334
DB 4625 AAGAGTAGACATACGGCTGACCGGATTTTGGTTTAAATAAGGAGAGATTGATTCGTG 4566

RESULT 6

US-08-461-823-1
Sequence 1, Application US/08461823
Patent No. 5593840

GENERAL INFORMATION:

APPLICANT: Bhatnagar, Satish K.
APPLICANT: George Jr., Albert L.
APPLICANT: Nazarenko, Irina
TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OncorPharm, Inc.
STREET: 200 Perry Parkway
CITY: Gaithersburg
STATE: Maryland
COUNTRY: USA
ZIP: 20877

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,823
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/168,621
FILING DATE: 16-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,433
FILING DATE: 27-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Karta, Glenn E.
REGISTRATION NUMBER: 30,649
REFERENCE/DOCKET NUMBER: PA-0012 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301 527-2058
TELEFAX: 301 208-6997
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-461-823-1

Query Match 0.8%; Score 52.4; DB 1; Length 2726;
Best Local Similarity 46.7%; Pred. No. 3.6e-05;
Matches 253; Conservative 0; Mismatches 211; Indels 18; Gaps 2;

QY 2750 AVGGCTGCACTGAATTTTATGAGGCCAGATCACCTCTCTCTGGGCCACATGGAG 2809
DB 1665 AGGGACTGAGCTGAGGTGAAGAAGGCCAGACGCTGCCTCTGTGGGACGATGGCT 1724
QY 2810 CGGGAAGACGACACCATGTCATCTGACGGGTGTTTCCCGCCGACCTCGGGCACCG 2869
DB 1725 GTGGGAAGAGACAGCTGTGTCAGCTCTCTGGAGCGGTCTACGACCCCTTGGCAGGAAAG 1784
QY 2870 CCTACATCTCTGGAAAGACAT---TCGCTCTGAGATGAGCACCATCGGCAGAACCTGG 2926
DB 1785 TGCTCTTGATGGCAAGAAATAAAGCGACTGAATGTTCACTGGCTCCGAGCACACCTGG 1844
QY 2927 GGGTCTGCCCCAGCATAACTGCTGCTTTTGACATGCTGACTGTCGAGAGACACATCTGGT 2986
DB 1845 GCATCGTCTCCCGAGGCCATCCTGTTTGTACTGCTGACGATTGCTGAGAACAATTGCTTATG 1904
QY 2987 TCTATGCCCGCTTGAAGGGCTCTCTGAGAAGCAGCTGAAGCGGAGATGGAGCAGATGG 3046
DB 1905 GAGACAACAGCGGGTGTGTCAGAGAGAGATCGTGAGGCGACAGAGAGGCCCAACA 1964
QY 3047 CCTGGATGTTGGTTGGCCATCAAGCAAGCTGAAAG-----CAAAACA 3091
DB 1965 TACATGCCCTTCATCGAGTCACTGGCTATAATAATAGCACTAAAGTAGGAGACAAGGAA 2024
QY 3092 GCCAGCTGTCAGTGAATCAGAGAAAGCTATCTGTGGCTTGGCTTGGCGGGGAT 3151
DB 2025 CTCAGCTCTCTGTGGCCAGAAACACCATGTCATAGCTGCTGCTCTGTTAGACAGC 2084
QY 3152 CTAGGTTGTCATCTGATGAACCCAGCAGCTGGTGTGGACCTTACTCCCGCAGGGAA 3211
DB 2085 CTCATATTTTGTCTTTGGATGAAGCCAGCTCAGCTCTGGATACAGAAAGTGAAGGTTG 2144
QY 3212 TATGGAGCTGCTGCTGAATACCGACAAGCGCCGACCATTTCTCTCTACACACACA 3271
DB 2145 TCCAGAAGCCCTGGACAAAGCCAGAGAGCGCCACCTGCTGCTGCTGCTGCTGCTGCTGCT 2204
QY 3272 TG 3273
DB 2205 TG 2206

RESULT 7

US-08-181-471-2
Sequence 2, Application US/08181471
Patent No. 5641508

GENERAL INFORMATION:

APPLICANT: Li, Liogna
APPLICANT: Lishko, Valery K.
TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas Fitting
STREET: 12526 High Bluff Drive, Suite 300
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92130
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,471
FILING DATE: 13-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,553
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: ANT0029P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-792-3680
TELEFAX: 619-792-8477
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 425..4267
US-08-181-471-2

Query Match 0.8%; Score 52.4; DB 1; Length 4646;
Best Local Similarity 46.7%; Pred. No. 5.5e-05;
Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;
QY 2750 ATGGCTGGCAGCTGAATTTTATGAGGGCCAGATCACTCTCTTCCTGGGCCAATGGAG 2809
DB 3585 AGGAGCTGAGCTGGAGGTGAAGAAGGCCAGACGCTGCTGTGGGAGCAGTGGCT 3644
QY 2810 CGGGAGAGCAGCACCATGTCATCTGACCGGTTGTCCTCCCGACCTCGGGCACCG 2869
DB 3645 GTGGAGAGCAGCAGTGGTCCAGCTCTCTGAGCGGTTCTACGACCTTGGCAGGAAAG 3704
QY 2870 CCTACATCTCGGAAAGACAT---TCGCTCTGAGATGAGCACCATCCGCGCAACCTGG 2926
DB 3705 TGTCTGTGATGCAAGAATAAAGGACTGATGTTTCAGTGGCTCCGAGCACACCTGG 3764
QY 2927 GGGTCTGTCCTCCAGCATGCTGCTGTGACATGCTGCTGCGAAGAACATCTGGT 2986
DB 3765 GCATCGTGTCCAGGAGCCATCTCTGTTGACTGACGATGCTGAGAACATTCCTATG 3824
QY 2987 TCTATGCCCTTTGAAAGGGCTCTCTGAGAGCAGTGAAGGGGAGATGGAGCAGATGG 3046
DB 3825 GAGACAACAGCGGGTGTGTACAGAGAGAGATCGTGAGGCGAAGAGGCGCAACA 3884
QY 3047 CCTGTGATGTTGGTTTCCATCAAGCAAGTGAAG---CAAACAA 3091
DB 3885 TACATGCTCTGAGTCACTGCTCTAATAATATAGCACTAAAGTAGGAGAGCAAGGAA 3944
QY 3092 GCCAGCTGTGAGTGAATGAGAGAAAGTATCTGTGGCTTGGCTTGTGGGGGAT 3151
DB 3945 CTCAGCTCTGTGGGCGCAAGAACAGCATTCGCATAGTCTGCTGCTGTTAGACAGC 4004
QY 3152 CTAGGTTGTCATCTGATGAACCCAGCAGTGGTGTGGACCTTATCTCCCGAGGGGAA 3211
DB 4005 CTCATATTTTCTTTGATGAAGCCAGCTGAGCTGTGGATACAGAAAGTGAAGAGTTG 4064
QY 3212 TATGGAGCTGCTGCTGAATACAGAGCCGCGCACCATTTCTCTACACACCA 3271
DB 4065 TCCAGAGAGCCCTTGACAAAGCCAGAGAGCCGCGCACCTGCTGATTTGCTCACCCTCC 4124
QY 3272 TG 3273

DB 4125 TG 4126
RESULT 8
US-08-583-276-18
Sequence 18, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
APPLICANT: Nienhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4659 bases
TYPE: nucleic acid
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: Genomic DNA
US-08-583-276-18

Query Match 0.8%; Score 52.4; DB 2; Length 4669;
Best Local Similarity 46.7%; Pred. No. 5.5e-05;
Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;
QY 2750 ATGGCTGGCAGCTGAATTTTATGAGGGCCAGATCACTCTCTTCCTGGGCCAATGGAG 2809
DB 3585 AGGAGCTGAGCTGGAGGTGAAGAAGGCCAGACGCTGCTGTGGGAGCAGTGGCT 3644
QY 2810 CGGGAGAGCAGCACCATGTCATCTGACCGGTTGTCCTCCCGACCTCGGGCACCG 2869
DB 3645 GTGGAGAGCAGCAGTGGTCCAGCTCTCTGAGCGGTTCTACGACCTTGGCAGGAAAG 3704
QY 2870 CCTACATCTCGGAAAGACAT---TCGCTCTGAGATGAGCACCATCCGCGCAACCTGG 2926
DB 3705 TGTCTGTGATGCAAGAATAAAGGACTGATGTTTCAGTGGCTCCGAGCACACCTGG 3764
QY 2927 GGGTCTGTCCTCCAGCATGCTGCTGTGACATGCTGCTGCGAAGAACATCTGGT 2986
DB 3765 GCATCGTGTCCAGGAGCCATCTCTGTTGACTGACGATGCTGAGAACATTCCTATG 3824
QY 2987 TCTATGCCCTTTGAAAGGGCTCTCTGAGAGCAGTGAAGGGGAGATGGAGCAGATGG 3046
DB 3825 GAGACAACAGCGGGTGTGTACAGAGAGAGATCGTGAGGCGAAGAGGCGCAACA 3884
QY 3047 CCTGTGATGTTGGTTTCCATCAAGCAAGTGAAG---CAAACAA 3091

Db 5037 GTGGGAAGACAGTGGTCCAGCTCCTGGAGCGGTTCTACGACCCCTTGGCAGGGAAG 5096
 QY 2870 CTTACATCCTGGGAAAGACAT---TCGCTCTGAGATGAGCACCACCTCCGGCAGACCTGG 2926
 Db 5097 TGTGCTTGTATGCAAGAAATAAAGCGACTGAATGTTTCAGTGGCTCCGAGCAGACCTGG 5156
 QY 2927 GGTGCTGTCCTCCAGCATAACGTGCTCTTTTGACATGCTGCTGGAAGAACACATCTGCT 2986
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 Db 5397 CTCATATTTTGTCTTTGGATGAAGCCACGCTACGCTCTGGATACAGAAAGTGAAGAGTTG 5456
 QY 3212 TATGGAGCTGCTGCTGAATACCGACAGCGCGCAGCACTATCTCTTACACACACA 3271
 Db 5457 TCCAGNAGCCCTGGACAAAGCCAGAGAGCGCGACCTCTGCTGCTGCTACCGCC 5516
 QY 3272 TG 3273
 Db 5517 TG 5518

RESULT 11

US-08-793-610-6
 ; Sequence 6, Application US/08793610
 ; Patent No. 5858744
 ; GENERAL INFORMATION:
 ; APPLICANT: BAUM, Christopher
 ; APPLICANT: STOCKING-HARBERS, Carol
 ; APPLICANT: OSTERTAG, Wolfram
 ; TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEREOF
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nikolaide, Marmelstein, Murray & Oram LLP
 ; STREET: 655 Fifteenth Street N.W. Suite 330
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-5701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/793,610
 ; FILING DATE: 07-MAR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 44 31 973.8
 ; FILING DATE: 08-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 195 03 952.1
 ; FILING DATE: 07-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP95/03175
 ; FILING DATE: 10-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Herman, Richard J.
 ; REGISTRATION NUMBER: 39,105

REFERENCE/DOCKET NUMBER: PI614-7007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)638-5000
 TELEFAX: (202)638-4810
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9318 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA
 US-08-793-610-6

Query Match 0.8%; Score 52.4; DB 2; Length 9318;
 Best Local Similarity 46.7%; Pred. No. 9.2e-05;
 Matches 253; Conservative 0; Mismatches 271; Indels 18; Gaps 2;
 QY 2750 ATGGCCCTGGCCTGATTTTATGAGGGCCAGATCACTCCTTCCTGGCCACATGAG 2809
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 Db 5356 CTCATATTTTGTCTTTGGATGAAGCCACGCTCAGCTCTGGATACAGAAAGTGAAGAGTTG 5415

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GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 16:38:15 ; Search time 429.143 Seconds
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13866.500 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

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- 13: /cgn2.6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2.6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	6766.4	99.7	9870	9	US-09-984-827-97
3	6766.4	99.7	9870	9	US-09-984-827-101
4	6766.4	99.7	9870	9	US-09-984-827-103
5	6766.4	99.7	9870	9	US-09-984-827-105
6	6764.8	99.7	9741	10	US-09-846-456-10
7	6764.8	99.7	9870	9	US-09-984-827-92
8	6764.8	99.7	9870	9	US-09-984-827-93
9	6764.8	99.7	9870	9	US-09-984-827-94
10	6764.8	99.7	9870	9	US-09-984-827-115
11	6764.8	99.7	9870	9	US-09-984-827-119
12	6764.8	99.7	9870	9	US-09-984-827-120
13	6764.8	99.7	9870	9	US-09-984-827-121
14	6764.8	99.7	9870	9	US-09-984-827-122
15	6764.8	99.7	9870	9	US-09-984-827-123
16	6764.8	99.7	9870	9	US-09-984-827-124
17	6764.8	99.7	9870	9	US-09-984-827-125
18	6764.8	99.7	9870	9	US-09-984-827-126
19	6763.2	99.7	9741	9	US-09-984-827-1

ALIGNMENTS

RESULT 1

US-09-984-827-95
Sequence 95, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: DENEPIE, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 95
LENGTH: 9870
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (7138)
OTHER INFORMATION: a, t, c or g
US-09-984-827-95

Query Match 99.7%; Score 6766.4; DB 9; Length 9870;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Db 314 ATGGCTTTGGCCTCAGCTGAGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGA 373

QY 61 CAAACATGTCAGCTGTACTGGAAGTGGCTGGCCCTTATTATCTCTGATCCCTGATC 120

Db 374 CAAACATGTCAGCTGTACTGGAAGTGGCTGGCCCTTATTATCTCTGATCCCTGATC 433

QY 121 TCTGTTGGCTGAGCTACCCATCCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 180
Db 434 TCTGTTGGCTGAGCTACCCATCCCTATGAACAACATGAATGCCATTTTCCAAATAAAGCC 493
QY 181 ATGCCCTCTCGAGGAACACATTCCTTGGGTTTCAGGGGATATCTGTAAATGCAACAACCC 240
Db 494 ATGCCCTCTCGAGGAACACATTCCTTGGGTTTCAGGGGATATCTGTAAATGCAACAACCC 553
QY 241 TGTTCCTGTTACCGGACTCTCGGGAGGCTCCGGAGTTTGGGAACATTTAAACAATCC 300
Db 554 TGTTCCTGTTACCGGACTCTCGGGAGGCTCCGGAGTTTGGGAACATTTAAACAATCC 613
QY 301 ATTGTGGCTCGCTGTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC 360
Db 614 ATTGTGGCTCGCTGTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC 673
QY 361 AGCATGAAGACATGCGCAAGTTCTGAGAACATTAACAGACATCAAGAAATCCAGCTCA 420
Db 674 AGCATGAAGACATGCGCAAGTTCTGAGAACATTAACAGACATCAAGAAATCCAGCTCA 733
QY 421 AACTTGAAGCTTCAAGATTTCCCTGGTGGACAATGAACCTTCTCTGGGTTCTATATAC 480
Db 734 AACTTGAAGCTTCAAGATTTCCCTGGTGGACAATGAACCTTCTCTGGGTTCTATATAC 793
QY 481 AACTCTCTCTCCCAAGTCTACTGTGGACAAAGATGCTGAGGCTGATGTCAATTCCTCCAC 540
Db 794 AACTCTCTCTCCCAAGTCTACTGTGGACAAAGATGCTGAGGCTGATGTCAATTCCTCCAC 853
QY 541 AAGSTATTTTTCAGGCTACCAAGTTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 600
Db 854 AAGSTATTTTTCAGGCTACCAAGTTTACATTTGACAAGTCTGTGCAATGGATCAAAATCA 913
QY 601 GAAGAGATGATTCAACTTGGTGACCAAGAGTTTCTGAGCTTTGTGGCTTACCAAGAGAG 660
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QY 721 AGAACAATTAACCTTACATCTCCCTCCCGAGCAAGAGTCTGCTGAAGCCACAAAACA 780
Db 1034 AGAACAATTAACCTTACATCTCCCTCCCGAGCAAGAGTCTGCTGAAGCCACAAAACA 1093
QY 781 TTGCTGCATAGTTTGGGACTCTGGCCAGAGAGTGTTCAGCATGAGAAGCTGGAGTGAC 840
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Db 1334 GAAGATGCTGAACCTTCTATGACAACCTTACAACCTCTTACTGCAATGATTTGATGAAG 1393
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QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACAAGGCAAGGTGATGGCTGAGGTGAAC 1200
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Db 1574 CCCAAGATCTGACCTTCATGAGACACGCCAAGAAATGGACCTTGTCCGGATCTGTG 1633
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Db 1934 ATTACTCAGGAGCATTTGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGGACAT 1993
QY 1681 GACATGTGGAGAGGACAAATAAATCAAGATGGGTACTGGGACCTTGGCTCTCGAGCT 1740
Db 1994 GACATGTGGAGAGGACAAATAAATCAAGATGGGTACTGGGACCTTGGCTCTCGAGCT 2053
QY 1741 GACCCCTTTGAGAGACATCGGTACGTCTGGGGGGCTTCGCTACTTTCAGGATGTGGT 1800
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QY 1801 GAGCAGGCAATCATCAGGCTGTGACGGGCACCGAGAGAAACTGGTGTCTATATCAA 1860
Db 2114 GAGCAGGCAATCATCAGGCTGTGACGGGCACCGAGAGAAACTGGTGTCTATATCAA 2173
QY 1861 CAGATGCCCTATCCCTGTACGTTGATGACATCTTTTCGGGGTGATGAGCCGCTCAATG 1920
Db 2174 CAGATGCCCTATCCCTGTACGTTGATGACATCTTTTCGGGGTGATGAGCCGCTCAATG 2233
QY 1921 CCCCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGT 1980
Db 2234 CCCCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGCAATCGT 2293
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QY 5581 GTGGTGTCTTCTCTCATTTACTGTCTGTATCCAGTACAGATTTCTTATCAGGCCAGACCT 5640
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 QY 5701 AGAATTTCTGTGTGTGGAGGCGAGAAATCAGATCTTAGAAATCAAGAGTTGACGAAGATA 5760
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 QY 5761 TATAGAAGGAAGCGGAGCCCTGTGTGTGACAGATTTGCGTGGGCAATCTCTCTGTGTGAG 5820
 Db 6074 TATAGAAGGAAGCGGAGCCCTGTGTGTGACAGATTTGCGTGGGCAATCTCTCTGTGTGAG 6133
 QY 5821 TGCTTTGGGCTCTCTGGGAGTTAATGGGCTGGAATAATCATCAACTTTCAAGATGTTAAACA 5880
 Db 6134 TGCTTTGGGCTCTCTGGGAGTTAATGGGCTGGAATAATCATCAACTTTCAAGATGTTAAACA 6193
 QY 5881 GGAGATACCACTGTGTACAGAGGAGATGCTTTTCCCTTAACAAAAATAGTATCTTATCAAAAC 5940
 Db 6194 GGAGATACCACTGTGTACAGAGGAGATGCTTTTCCCTTAACAAAAATAGTATCTTATCAAAAC 6253
 QY 5941 ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6000
 Db 6254 ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6313
 QY 6001 TTGACTGGGAGAGAACACGTGGAGTTCTTTTCCCTTTTGGAGAGGAGTCCCGAGAGAAAGAA 6060
 Db 6314 TTGACTGGGAGAGAACACGTGGAGTTCTTTTCCCTTTTGGAGAGGAGTCCCGAGAGAAAGAA 6373
 QY 6061 GTTCGCAAGGTTGTGTGAGTGGGCGATTCGGAAGTTCGGCTCTGTGAAGTATGAGAGAAAA 6120
 Db 6374 GTTCGCAAGGTTGTGTGAGTGGGCGATTCGGAAGTTCGGCTCTGTGAAGTATGAGAGAAAA 6433
 QY 6121 TATCTGTTAACTATAGTGGAGGCAACAAAGCTCTCTACAGGCTAGCTTGTATC 6180
 Db 6434 TATCTGTTAACTATAGTGGAGGCAACAAAGCTCTCTACAGGCTAGCTTGTATC 6493
 QY 6181 GCGGGGCTCTGTGTGTCTGTGATGAACCCACACAGGATGATCCCAAGGCGCGG 6240
 Db 6494 GCGGGGCTCTGTGTGTCTGTGATGAACCCACACAGGATGATCCCAAGGCGCGG 6553
 QY 6241 CGGTCTCTGTGGAATTTGCCCTAAGTGTGTCAAGGAGGAGATCAGTAGTGTATACA 6300
 Db 6554 CGGTCTCTGTGGAATTTGCCCTAAGTGTGTCAAGGAGGAGATCAGTAGTGTATACA 6513
 QY 6301 TCTCATAGTATGAAGAAATGTGAAGTCTTTGCACTAGGATGGAATCATGTGCAATGA 6360
 Db 6614 TCTCATAGTATGAAGAAATGTGAAGTCTTTGCACTAGGATGGAATCATGTGCAATGA 6673
 QY 6361 AGGTTCAGGTGCTTGGCAGTGTCCAGCTATCAAAATAGGTTTGGAGATGTTTATACA 6420
 Db 6674 AGGTTCAGGTGCTTGGCAGTGTCCAGCTATCAAAATAGGTTTGGAGATGTTTATACA 6733
 QY 6421 ATAGTTGTAGAAATAGAGGTTCCAAACCGGAGCTTGAAGCTTGTCCAGGATTTCTTTGGA 6480
 Db 6734 ATAGTTGTAGAAATAGAGGTTCCAAACCGGAGCTTGAAGCTTGTCCAGGATTTCTTTGGA 6793
 QY 6481 CTTCATTTCTCGAAGTGTCTTAAAGAGAAACCCGGAACATGCTACAATACAGCTT 5540
 Db 6794 CTTCATTTCTCGAAGTGTCTTAAAGAGAAACCCGGAACATGCTACAATACAGCTT 5853
 QY 6541 CCATCTTCATTTCTCTCTGGCCAGGATATTCAGATCTCTCCAGAGCAAAAAGCGA 5600
 Db 6854 CCATCTTCATTTCTCTCTGGCCAGGATATTCAGATCTCTCCAGAGCAAAAAGCGA 6913
 QY 6601 CTCACATAGAAAGTACTCTGTTTCTCAGACAAACTTGACCAGATTTGTGAACTTT 6660
 Db 6914 CTCACATAGAAAGTACTCTGTTTCTCAGACAAACTTGACCAGATTTGTGAACTTT 6973
 QY 6661 GCCAAGGACCAAGTATGATGATGACCACTTTAAAAGACCTCTCTCATTTACACAAAAACAGCA 6720

Db 6974 GCCAAGGACCAAGTGGATGACCACTAAAGAGCCTCTATTACAAAACACAGACA 7033
QY 6721 GTAGTGGAGTTCAGTCTACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
Db 7034 GTAGTGGAGTTCAGTCTACATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 7093
QY 6781 GTAT 6784
Db 7094 GTAT 7097

RESULT 2
US-09-984-827-97
; Sequence 97, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSTER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIONE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984, 827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-97

Query Match 99.7%; Score 6766.4; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGCTTTGGGCTCAGCTGAGGTTCCTCTGGAAGAACCTCATTTCAGAAAGA 60
Db 314 ATGGCTTTGGGCTCAGCTGAGGTTCCTCTGGAAGAACCTCATTTCAGAAAGA 373
QY 61 CAACATGTCAGCTGTCTGAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 120
Db 374 CAACATGTCAGCTGTCTGAGTGGCTGGCTCTATTATCTTCCTGATCCTGATC 433
QY 121 TCTGTTCCGGTGGAGTACCAACCTATGACACATGAATGCCATTTTCCAAATAAGCC 180
Db 434 TCTGTTCCGGTGGAGTACCAACCTATGACACATGAATGCCATTTTCCAAATAAGCC 493
QY 181 ATGCCCTCTCAGAAACATCTCTGTTGGTTCAGGGATTATCTGTAATGCCAACACCCC 240
Db 494 ATGCCCTCTCAGAAACATCTCTGTTGGTTCAGGGATTATCTGTAATGCCAACACCCC 553
QY 241 TGTGTTCCGGTACCGGACTCCTGGGAGGCTCCCGAGTGTGTTGAAACTTTTAAATAATCC 300
Db 554 TGTGTTCCGGTACCGGACTCCTGGGAGGCTCCCGAGTGTGTTGAAACTTTTAAATAATCC 613
QY 301 ATTTGGGCTCCGCTGTTCTAGATGCTCGGAGGCTCTTTTATACAGCCAGAGACACC 360
Db 614 ATTTGGGCTCCGCTGTTCTAGATGCTCGGAGGCTCTTTTATACAGCCAGAGACACC 673
QY 361 AGCATGAAGGACATGCGCAAGTTCAGAACATTACAGAGATCAAGAAATCCAGCTCA 420

Db 674 AGCATGAAGGACATGCGCAAGTTCAGAACATTACAGCAGATCAAGAAATCCAGCTCA 733
QY 421 AACTTGAAGCTTCAAGATTCTCTGGTGGACAAATGAACCTTCTCTGGTTCCTATATAC 480
Db 734 AACTTGAAGCTTCAAGATTCTCTGGTGGACAAATGAACCTTCTCTGGTTCCTATATAC 793
QY 481 AACTCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGGCTGATGTCATTCTCCAC 540
Db 794 AACCTCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGAGGGCTGATGTCATTCTCCAC 853
QY 541 AAGGTATTTTTCGAAGGCTACCAAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA 600
Db 854 AAGGTATTTTTCGAAGGCTACCAAGTTACATTTGACAAAGTCTGTGCAATGGATCAAAATCA 913
QY 601 GAAGAGATGATCAACTTGGTGACCAAGATTTCTGAGCTTTGCGCTACCAAGAGAG 660
Db 914 GAAGAGATGATCAACTTGGTGACCAAGATTTCTGAGCTTTGCGCTACCAAGAGAG 973
QY 661 AAATCGGCTGCAGCAGAGCGAGTACTTCTGTTCCCAACATGGACATCCTGAAAGCTG 720
Db 974 AAATCGGCTGCAGCAGAGCGAGTACTTCTGTTCCCAACATGGACATCCTGAAAGCTG 1033
QY 721 AGAACATAAATCTACATCTCCCTCCGAGCAGAGCTGGCTGAGCCACACAAACAA 780
Db 1034 AGAACATAAATCTACATCTCCCTCCGAGCAGAGCTGGCTGAGCCACACAAACAA 1093
QY 781 TTGCTGCTAGTCTGGGACTCTGCCAGGAGCTGTTTCCAGCATGAGAAGCTGGAGTGAC 840
Db 1094 TTGCTGCTAGTCTGGGACTCTGCCAGGAGCTGTTTCCAGCATGAGAAGCTGGAGTGAC 1153
QY 841 ATGCGACAGGAGGTGATGTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC 900
Db 1154 ATGCGACAGGAGGTGATGTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCCAAATC 1213
QY 901 TACCAGGCTGTCTGCTGATTGCTGCGGCGATCCCGAGGAGGGGGCTGAAGATCAAG 960
Db 1214 TACCAGGCTGTCTGCTGATTGCTGCGGCGATCCCGAGGAGGGGGCTGAAGATCAAG 1273
QY 961 TCTCTCACTGTATGAGGACAACTACAAAGCCCTCTTTTGGAGGCAATGGCTGAG 1020
Db 1274 TCTCTCACTGTATGAGGACAACTACAAAGCCCTCTTTGGAGGCAATGGCTGAG 1333
QY 1021 GAAGATGCTGAACCTTCTATGACAACTTACAACTCTTACTGCAATGATTGATGAAG 1080
Db 1334 GAAGATGCTGAACCTTCTATGACAACTTACAACTCTTACTGCAATGATTGATGAAG 1393
QY 1081 AATTGGAGTCTAGTCTCTCTTCCCGCATTTATCTGAAAGCTCTGAAAGCCGTGCTGTT 1140
Db 1394 AATTGGAGTCTAGTCTCTCTTCCCGCATTTATCTGAAAGCTCTGAAAGCCGTGCTGTT 1453
QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACAAAGCAGGTGATGCTGAGGTGAAC 1200
Db 1454 GGAAGATCCTGTATACACTGACACTCCAGCCACAAAGCAGGTGATGCTGAGGTGAAC 1513
QY 1201 AAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGGATGTTGGAGGAACCTCAGC 1260
Db 1514 AAGACCTTCCAGGAACTGGCTGTGTTCCATGATCTGGAAGGATGTTGGAGGAACCTCAGC 1573
QY 1261 CCCAAGATCTGACCTTCATGGAAGACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1320
Db 1574 CCCAAGATCTGACCTTCATGGAAGACAGCCAAAGAAATGGACCTTGTCCGGATGCTGTTG 1633
QY 1321 GACAGCAGGACAAATGACCACTTTTGGGAACAGCAGTGTGATGGCTTAGATTGGACAGCC 1380
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QY 1381 CAAGACATCTGGCGTTTTTGGCCAAAGCAGAGATGTCCAGTCCAGTAAATGTTCT 1440
Db 1694 CAAGACATCTGGCGTTTTTGGCCAAAGCAGAGATGTCCAGTCCAGTAAATGTTCT 1753
QY 1441 GTGTACACCTGGAGAGAGCTTTTCAAGGACACTAACCCAGGCAATCCGGACCATCTCCG 1500
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QY 1501 TTCAATGAGTGTGTCAACCTGAAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1560
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Db 1874 AACAAAGTCCATGGAGCTGTGGATGAGAGGAAGTTCCTGGCTGGTATGTGTTCACATGGA 1933
QY 1621 ATTACTCCAGGCACATGAGCTGCCCATCATGCTCAAGTACAGATCCCAATGGACATT 1680
Db 1934 ATTACTCCAGGCACATGAGCTGCCCATCATGCTCAAGTACAGATCCCAATGGACATT 1993
QY 1681 GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGACCCCTGGTCTCGAGCT 1740
Db 1994 GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGACCCCTGGTCTCGAGCT 2053
QY 1741 GACCCCTTTGAGGACATGCGGTACGTCTGGGGGCTTCGCCCTACTTTCAGAGATGTGGT 1800
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QY 1801 GAGCAGCAATCATCAGGCTGCTGAGGGCACCAGAGAGAAACTGGTGTATATGCAA 1860
Db 2114 GAGCAGCAATCATCAGGCTGCTGAGGGCACCAGAGAGAAACTGGTGTATATGCAA 2173
QY 1861 CAGATGCCCTATCCCTGTACGTGTGATGACATCTTTCTCGGGGTGATGACCGGTCAATG 1920
Db 2174 CAGATGCCCTATCCCTGTACGTGTGATGACATCTTTCTCGGGGTGATGACCGGTCAATG 2233
QY 1921 CCCTCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGG 1980
Db 2234 CCCTCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGG 2293
QY 1981 TATGAGAGGAGGACGCGGTGAAGAGACCATGCGGATCATGGGCTGGACACAGCAT 2040
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QY 2041 CTCTGGTTTACGTGTGTATAGTACCTTACTTCCCTTCTTGTGAGCGCTGGCCTGCTA 2100
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QY 2401 GGCATTGGAGTGCATGGACAACTGTTCAGAGTCTCTGGAGAGAGATGGCTTCAAT 2460
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QY 2581 ACCAAGTCTACTGTTTGGCAGGAGAAAGTGTAGAGAGAGCCACCTGGTTTCCAAACAG 2640
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QY 2821 ACCACATGTCAATCCTGACCGGTTGTTCCCGGACCTCGGGCACCCTACATCTG 2880
Db 3134 ACCACATGTCAATCCTGACCGGTTGTTCCCGGACCTCGGGCACCCTACATCTG 3193
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QY 3121 CTATCTGTGGCTTGGCTTGTGCGGGATCTAAGTGTGATTCATCTGGATGAACCCACA 3180
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QY 3301 ATTGCCATCATCTCCATGGGAACTGTGCTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3360
Db 3614 ATTGCCATCATCTCCATGGGAACTGTGCTGTGGGCTCCTCCCTGTTTCTGAAGAAC 3673
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 Db 6434 TATGCTGGTAACATATAGTGGAGGCAACAAACGCAAGCTCTACAGCCATGCTTTGATC 6493
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 Db 6494 GCGGGGCTCCTGTGTGTTCTGGATGAACCCACAGGATGATCCCAAGGCCGG 6553
 QY 6241 CGGTTCTTGGGAATGTGCGCTTAACTGTGTCAGGAGGGGATCAGTAGTCTTACA 6300
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 QY 6361 AGGTTTCAGTGTGCTGGAGTGTCCAGCTCTTAAAGAAATAGTTTGGAGATGGTTATACA 6420
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 Db 6734 ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGAAGCCCTGTCAGGATTTCTTGA 6793
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 Db 6794 CTGCAATTTCTGGAGTGTCTTAAAGAGAAACACCGGACATGCTACATACACAGCTT 6853
 QY 6541 CCATCTTCATTTATCTCTGCGCAGGATATTCAGATCTCTCCAGAGCAAAAGCGA 6600
 Db 6854 CCATCTTCATTTATCTCTGCGCAGGATATTCAGATCTCTCCAGAGCAAAAGCGA 6913
 QY 6601 CTCACATAGAGACTACTCTGTTCTCAGACAAACACTTGACCAAGTATTTGTGAACCTT 6660
 Db 6914 CTCACATAGAGACTACTCTGTTCTCAGACAAACACTTGACCAAGTATTTGTGAACCTT 6973
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 QY 6721 GTAGTGGAGCTTGGAGTCTCAGTCTTCTCAGAGCAACACTTGACCAAGTATTTGTGAACCTT 6780
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 QY 6781 GTAT 6784
 Db 7094 GTAT 7097

RESULT 3
 US-09-984-827-101
 ; Sequence 101, Application US/09984827
 ; Publication No. US2003005623A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DENEFLÉ, PATRICE
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
 ; APPLICANT: DUVERGER, NICOLAS
 ; APPLICANT: CAMBIEN, FRANCOIS
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
 ; FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
 ; FILE REFERENCE: 03806.0522-00000
 ; CURRENT APPLICATION NUMBER: US/09/984,827
 ; CURRENT FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 60/254,108
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: FR 00/14037
 ; PRIOR FILING DATE: 2000-10-31
 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 101
 ; LENGTH: 9870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (7138)
 ; OTHER INFORMATION: a, t, c or g
 US-09-984-827-101

Query Match 99.7%; Score 6766.4; DB 9; Length 9870;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGCTTCTTGGCCTCAGCTGAGGTGCTGTGGAGAACCTCCTTTCAGAGAGA 60
 Db 314 ATGGCTTCTTGGCCTCAGCTGAGGTGCTGTGGAGAACCTCCTTTCAGAGAGA 373
 QY 61 CAACATGTCAGCTGTGTTACTGGAAGTGGCCTGCTTATTTATCTTCTGATCCTGATC 120
 Db 374 CAACATGTCAGCTGTGTTACTGGAAGTGGCCTGCTTATTTATCTTCTGATCCTGATC 433
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 Db 434 TCTGTGGCTGAGCTACCCACCCTATGACACATCAATGCCATTTTCCAAATAAGCC 493
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 Db 614 ATTGTGCTGCTGCTTCTCAGATGCTCGGAGGCTTCTTTTATACAGCCAGAAAGACACC 673
 QY 361 AGCATGAAGACATGCCCAAGTCTCAGAACATTCAGACAGATCAAGAATCCAGCTCA 420
 Db 674 AGCATGAAGACATGCCCAAGTCTCAGAACATTCAGACAGATCAAGAATCCAGCTCA 733
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 Db 734 AACTTGAAGCTTCAAGATTTCTTGGTGCAATCAACCTTCTCTGGTTTCTTATATAC 793
 QY 481 AACTTCTCTCCAAAGTCTACTGTGGCAAGATGCTGAGGCTGATGTCATTTCCAC 540
 Db 794 AACTTCTCTCCAAAGTCTACTGTGGCAAGATGCTGAGGCTGATGTCATTTCCAC 853
 QY 541 AAGGTATTTTGAAGGCTACCAAGTTTACATTTTACAGTCTGTCATGATGATCAATCA 600
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Db 974 AAACCTGGCTGCACAGAGCGAGTACTGGTTCCACATGGACATCTGAAGCAATCCCTG 1033
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QY 781 TTGCTGCATAGTCTTGGACTCTGGCCAGGAGCTCTTCAGCATGAGAGCTGGAGTGAC 840
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Db 1214 TACCAGCTCTCTCGTATGTTCTGGGGCAATCCCGAGGAGGGGGCTGAGATCAAG 1273
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Db 1274 TCTCTCAACTGGTATGAGGACAACAATAAAGCCCTCTTTGGAGSCAATGGCACTGAG 1333
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Db 1334 GAGATGCTGAACCTTCTATGACACTCTACAACTCCCTTACTGCAATGATTTGATGAAG 1393
QY 1081 AATTGGAGTCTAGTCTCTCTTCCCGCATATCTGGAAGCTCTGAAGCCCTGCTCGTT 1140
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QY 1321 GACAGCAGGACATGACCACTTTTGGGAACGCAGTTGGATGGCTTAGATTTGACAGACC 1380
Db 1634 GACAGCAGGACATGACCACTTTTGGGAACGCAGTTGGATGGCTTAGATTTGACAGACC 1693
QY 1381 CAAGACATCTGGGCTTTTGGCCAAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT 1440
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Db 1934 ATTACTCCAGGACATGAGCTGCCCATCATCTCAAGTACAAGATCCGAATGGACATT 1993
QY 1681 GACAATGTGGAGGACAAATFAAATCAAGGATGGTACTGGGACCCTGTCTCCGAGCT 1740
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Db	5414	TCFAATTTGTCTGGGATATGTGCAAATPAGTTGTCCCTGCCACACTGTGCTAATATCATC	5473
QY	5161	TTCATCTGCTCCAGCAGAAAGTCTATGTGTCTCTCCACCAATCTGCCTGTGCTAGCCCTT	5220
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QY	5221	CTACTTTTGTGTATGGTGGTCAATCACACCTCTCATGTACCGACGCTCCTTTTGTGTTT	5280
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QY	5281	AAGATCCCAGCAGACCTATGTGGTCTCACACAGCTGAACCTCTTCATTTGGCATTAAAT	5340
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QY	5341	GGCAGCTGGCCACCTTTGTGCTGGAGCTGTTCCACGACAAATAGCTGAATAATATCAAT	5400
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QY	5521	GTGTACCATATATCTTGGGACTTGGTGGGAGAAACCTCTTGCCTGGCCGTGGGAAGG	5580
Db	5834	GTGTACCATATATCTTGGGACTTGGTGGGAGAAACCTCTTGCCTGGCCGTGGGAAGG	5893
QY	5581	GTGTGTTCTTCCCTCATCTACTGTTCTGATCCAGTACAGATTTCTTCATCAGGCCACCT	5640
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QY	5641	GTAATGCAAAAGCTATCTCCTCTCAATGATCAAGATGAAGTGTAGCGGGAAGACAG	5700
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QY	5761	TATAGAAGAAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGCATCTCCTCTGTTGAG	5820
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QY	5881	GGAGATACCACTGTTACAGAGGAGATGCTTTCTTTACAAAAATAGTATCTTATCAAC	5940
Db	6194	GGAGATACCACTGTTACAGAGGAGATGCTTTCTTTACAAAAATAGTATCTTATCAAC	6253
QY	5941	ATCCATGAGTACATCAGAAATGGCTACTGCTCCTCAGTTTGATGCCATCACAGAGCTG	6000
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QY	6061	GTGGAAGGTTGGTGAAGTGGCGATTCGGAACCTGGGCTCGTCAAGTATGAGAGAAAA	6120
Db	6374	GTGGAAGGTTGGTGAAGTGGCGATTCGGAACCTGGGCTCGTCAAGTATGAGAGAAAA	6433
QY	6121	TATGCTGGTAACTATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGGCTTTGATC	6180

6434	Db	TATGCTGGTAACATATAGTGGAGGCAACAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6493
6181	Qy	GGCGGGCTCCTGTGGTCTTTCTGGATGAACCCACACAGGCGATGGATCCCAAGACCCGG	6240
6494	Db	GGCGGGCTCCTGTGGTGTCTTCTGGATGAACCCACACAGGCGATGGATCCCAAGACCCGG	6553
6241	Qy	CGTTTCTGTGGAATTGTGCCCTTAAGTGTGTCAAGGAGGGGAGATCAGTAGTCTTACA	6300
6554	Db	CGTTTCTGTGGAATTGTGCCCTTAAGTGTGTCAAGGAGGGGAGATCAGTAGTCTTACA	6613
6301	Qy	TCTCATAGTATGGAAGAATGTGAAGTCTTTGACCTAGATGCCAATCATGGTCAATGGA	6360
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6361	Qy	AGTTTCAGGTGCCCTGGCAGTGTCCAGCATCTFAAAAAATAGCTTTGGAGATGGTTATACA	6420
6674	Db	AGTTTCAGGTGCCCTGGCAGTGTCCAGCATCTFAAAAAATAGCTTTGGAGATGGTTATACA	6733
6421	Qy	ATAGTTGTACGAATAGCAGGGTCCAAACCCGGACCTCAAGCCTCTCCAGAGATTTCTTTGGA	6480
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6481	Qy	CTTGCAATTCCTGGAAGTGTCTFAAAGAGAAACACCCGGACCTCTCCAGAGATTTCTTTGGA	6540
6794	Db	CTTGCAATTCCTGGAAGTGTCTFAAAGAGAAACACCCGGACCTCTCCAGAGATTTCTTTGGA	6853
6541	Qy	CCATCTTCATATATCTCTCTGGCCAGGATATTCAGCATCTCTCCAGAGATTTCTTTGGA	6600
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6601	Qy	CTCCACATAGAAGACTACTCTGTTTCTCAGAACACCTTGACCAAGATTTTGTGAACCTTT	6660
6914	Db	CTCCACATAGAAGACTACTCTGTTTCTCAGAACACCTTGACCAAGATTTTGTGAACCTTT	6973
6661	Qy	GCCAGGACCAAGGATGATGACCACTTAAAGACCTCTCATTACACAAAACCCAGACA	6720
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6721	Qy	GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAGAACCTAT	6780
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RESULT 4			
US-09-984-827-103			
; Sequence 103, Application US/09984827			
; Publication No. US20030056234A1			
; GENERAL INFORMATION:			
; APPLICANT: DENEFELE, PATRICE			
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE			
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE			
; APPLICANT: DUVERGER, NICOLAS			
; APPLICANT: CAMBIEN, FRANCOIS			
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR			
; FILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR			
; FILE REFERENCE: 03806.0522-00000			
; CURRENT APPLICATION NUMBER: US/09/984.827			
; CURRENT FILING DATE: 2002-04-01			
; PRIOR APPLICATION NUMBER: 60/254,108			
; PRIOR FILING DATE: 2000-12-11			
; PRIOR APPLICATION NUMBER: FR 00/14037			
; PRIOR FILING DATE: 2000-10-31			
; NUMBER OF SEQ ID NOS: 161			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 103			
; LENGTH: 9870			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			

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RESULT 4
US-09-984-827-103
; Sequence 103, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
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; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 103
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-103

Query Match 99.7%; Score 6766.4; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGCTGTGGCTCAGCTGAGTTCCTGCTGTGGAAGAACCTCCTCCTCAGAAAGA 60
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DB 2294 TATGAGAGGAGGACCGGCTGAAAGAGACCATCGGATCATGGGCTTGACAAACAGCAT 2353
QY 2041 CTCGTGTTAGCTGTTCAATTAGTAGCCTCATCTCTTCTTGTGAGCGCTGGCTGCTA 2100

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Qy	2101	 GTGGTCAT CCTCAAGT TAGGAAAC CTGCTGCT GCTTACAG TATCCAGC AGCTGTGT GTGTTC	2160
Db	2414	 GTGGTCAT CCTGAGGT TAGGAAAC CTGCTGCC TTCAGTAT CCAGAGCT GTGTGTTC	2473
Qy	2161	 TTCTGTCC GTGTTTGC TGTGTGGT TGACAACT CTGCAGTG CTCTCTGT ATTAGCAC ATCTTC	2220
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Qy	2221	 TTCAGAGC CAACCTGC GACGACCT GTGGGGCA TCATCTAC TTACGCTG ATGATGAC CTGCCC	2280
Db	2534	 TTCAGAGC CAACCTGC GACGACCT GTGGGGCA TCATCTAC TTACGCTG ATGATGAC CTGCCC	2593
Qy	2281	 TAGCTCCT GTGTGSCA TGTGGCAT GTGGGCTT CCACATCA AGATCTTC GCTATG	2340
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Qy	2341	 CTGCTGTC CTCTGTGC CTTTGGGT TTGGCTGT GAGTACTT TGCCCTTT TTTGGAGG ACAG	2400
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Qy	2461	 CTCACACAT TTCGATCT CCATGATG TGTTTGAC ACCTTCTC TATGGGTG ATGACCTG	2520
Db	2774	 CTCACACAT TTCGATCT CCATGATG TGTTTGAC ACCTTCTC TATGGGTG ATGACCTG	2833
Qy	2521	 TACATTGA GGCTGCTC TTTCCAGC GCAGTACG GAATTCCT CCAGGCCCT GGTATTTCT	2580
Db	2834	 TACATTGA GGCTGCTC TTTCCAGC GCAGTACG GAATTCCT CCAGGCCCT GGTATTTCT	2893
Qy	2581	 ACCAAGTC CTACTGTT TGGCGAGG AAAGTGAT GAGAAAGC CACTGCTGT GATCCACAC	2640
Db	2894	 ACCAAGTC CTACTGTT TGGCGAGG AAAGTGAT GAGAAAGC CACTGCTGT GATCCACAC	2953
Qy	2641	 AAGAGATG TCACAAAT CTGCATGG AGGAGGAAC CCACCCACT TTGAAGCTG GGCGTGTCC	2700
Db	2954	 AAGAGATG TCACAAAT CTGCATGG AGGAGGNA CCCCACCT TTGAAGCTG GGCGTGTCC	3013
Qy	2701	 ATTCAGAAC CTGGTAAAG TCTACCGAG ATGGGATG GAAGTGGCT GTGCGATG GCGCTGGCA	2760
Db	3014	 ATTCAGAAC CTGGTAAAG TCTACCGAG ATGGGATG GAAGTGGCT GTGCGATG GCGCTGGCA	3073
Qy	2761	 CTGAATTT TTTATGAGG CCAGATCAC CTCTTCTCT TGCGCCAC AATGAGCGG GGAAGACG	2820
Db	3074	 CTGAATTT TTTATGAGG CCAGATCAC CTCTTCTCT TGCGCCAC AATGAGCGG GGAAGACG	3133
Qy	2821	 ACCACCAT GTCAATCT GTGACCTG ACCGGGTT TTTCCCGC CGACCTGGC GACCGCTAT	2880
Db	3134	 ACCACCAT GTCAATCT GTGACCTG ACCGGGTT TTTCCCGC CGACCTGGC GACCGCTAT	3193
Qy	2881	 GGAAAGAC ATTTGCTG TAGATGAC CACCATTCC CGCGAGAC CTTGGGGGT CTGTCCCCAG	2940
Db	3194	 GGAAAGAC ATTTGCTG TAGATGAC CACCATTCC CGCGAGAC CTTGGGGGT CTGTCCCCAG	3253
Qy	2941	 CATACGTC GTGTTGAC ATGCTGACT GTGCGAAG AACACATCT GTGTTTATG TCGCCCGTTG	3000
Db	3254	 CATACGTC GTGTTGAC ATGCTGACT GTGCGAAG AACACATCT GTGTTTATG TCGCCCGTTG	3313
Qy	3001	 AAAGGGCT CTCTGAGA GACAGTGA AGCGGAGAT GTGGAGCAG ATGGCCCTG GGATTTGGT	3060
Db	3314	 AAAGGGCT CTCTGAGA GACAGTGA AGCGGAGAT GTGGAGCAG ATGGCCCTG GGATTTGGT	3373
Qy	3061	 TTGCCATC AAGCAAGC TGAAGCA AAACAAAGC ACGCTGTCA GGTGAATG CAAGAAAG	3120
Db	3374	 TTGCCATC AAGCAAGC TGAAGCA AAACAAAGC ACGCTGTCA GGTGAATG CAAGAAAG	3433
Qy	3121	 CTATCTGT GGCCTTGT GTGGGGAT CTTAAGGT TTGTCATTT CTTGATGA ACCCACA	3180

[illegible]

QY	5341	GGCAGCTGGCCACCTTTGTCTGGAGCTGTTCACCGGACAATAAGCTGAATAATATCAAT	5400
Db	5654	GGCAGCTGGCCACCTTTGTCTGGAGCTGTTCACCGGACAATAAGCTGAATAATATCAAT	5713
QY	5401	CATATCCTGAAGTCGCGTGTCTTTGATCTTCCACATTTTTCCTGGGACGAGGGCTCATC	5460
Db	5714	GATATCCTGAAGTCGCGTGTCTTTGATCTTCCACATTTTTCCTGGGACGAGGGCTCATC	5773
QY	5461	GACATGGTGA AAAACACAGGCAATGGCTGATGCCCTGGAAAGTTTTCGGGAGAAATCGCTTT	5520
Db	5774	GACATGGTGA AAAACACAGGCAATGGCTGATGCCCTGGAAAGTTTTCGGGAGAAATCGCTTT	5833
QY	5521	GTGTACCATATATCTTGGGACTTTGGTGGACGAAACCTCTTCGCCATGGCCGTGGAAGG	5580
Db	5834	GTGTACCATATATCTTGGGACTTTGGTGGACGAAACCTCTTCGCCATGGCCGTGGAAGG	5893
QY	5581	GTGTGTGTCTTCTCATCTACTGTCTGATGCCAGTACAGATTCCTTCATCAGGCCACAGCCT	5640
Db	5894	GTGTGTGTCTTCTCATCTACTGTCTGATGCCAGTACAGATTCCTTCATCAGGCCACAGCCT	5953
QY	5641	GTAATCAAAAGCTATCTCCTCTCAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5700
Db	5954	GTAATCAAAAGCTATCTCCTCTCAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	6013
QY	5701	AGAAATCTTGATGGTGGAGGCCAGAAATGACATCTTAGAAATCAAGAGGTTGACGNAGATA	5760
Db	6014	AGAAATCTTGATGGTGGAGGCCAGAAATGACATCTTAGAAATCAAGAGGTTGACGNAGATA	6073
QY	5761	TATAGAAGGAAGCGGAAGCCCTGCTGTGTACAGGATTCGGTGGGCATTCCTCCTGGTGAG	5820
Db	6074	TATAGAAGGAAGCGGAAGCCCTGCTGTGTACAGGATTCGGTGGGCATTCCTCCTGGTGAG	6133
QY	5821	TGCTTTGGGCTCCTGGAGTTAATGGGCTGGAAATCATCACTTCCAAGATCTTACACA	5880
Db	6134	TGCTTTGGGCTCCTGGAGTTAATGGGCTGGAAATCATCACTTCCAAGATCTTACACA	6193
QY	5881	GGAGATACCACTGTTACGAGGAGATGCTTTCCCTTAACAAAAATAGTATCTTATCAAC	5940
Db	6194	GGAGATACCACTGTTACGAGGAGATGCTTTCCCTTAACAGAAATAGTATCTTATCAAC	6253
QY	5941	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG	6000
Db	6254	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG	6313
QY	6001	TTGACTGGGAGAACACGTGGAGTTCTTTTGCCCTTTTGAGAGGAGTCCGACAGAAAGAA	6060
Db	6314	TTGACTGGGAGAACACGTGGAGTTCTTTTGCCCTTTTGAGAGGAGTCCGACAGAAAGAA	6373
QY	6061	GTTGGCAAGGTTTGCTGAGTGGGCGATTCGGAACATGGGCTCGTGAAGTATGGAGAAAA	6120
Db	6374	GTTGGCAAGGTTTGCTGAGTGGGCGATTCGGAACATGGGCTCGTGAAGTATGGAGAAAA	6433
QY	6121	TATGCTGGTAACTATAGTGGAGGCAACAACCGCAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6434	TATGCTGGTAACTATAGTGGAGGCAACAACCGCAGCTCTCTACAGCCATGGCTTTGATC	6493
QY	6181	GGCGGGCTCCTGTGTGTTCCTGGATGAACCCACACAGGCATGGATCCCAAGACCCCGG	6240
Db	6494	GGCGGGCTCCTGTGTGTTCCTGGATGAACCCACACAGGCATGGATCCCAAGACCCCGG	6553
QY	6241	CGGTTCTTTGGAAATGTGCCCTTAAGTGTGTTCAGGAGGGGAGATCAGTAGTCTTACACA	6300
Db	6554	CGGTTCTTTGGAAATGTGCCCTTAAGTGTGTTCAGGAGGGGAGATCAGTAGTCTTACACA	6613
QY	6301	TCTCATAGTATGGAAGAAATGTGAAGCTCTTTGCACCTAGGATGGCAATCATGGTCAANTGGA	6360
Db	6614	TCTCATAGTATGGAAGAAATGTGAAGCTCTTTGCACCTAGGATGGCAATCATGGTCAANTGGA	6673
QY	6361	AGGTTTCAGGTGCCCTTGGCAGTGTCCACGATCTAAAAAATAGGTTTGGAGATGGTTATACA	6420
Db	6674	AGGTTTCAGGTGCCCTTGGCAGTGTCCACGATCTAAAAAATAGGTTTGGAGATGGTTATACA	6733
QY	6421	ATAGTTCTAGCAATAGCAGGGTCCAAACCCGGACCTGGAAGCCTGTCCAGGATTTCTTTGGA	6480

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Db 6734 ATAGTGTACGATAGAGGTCCTCAACCGGACCTGGAAGCCGTGTCAGGATTTCTTTGGA 6793
QY 6481 CTTGCAATTCCTGGAAGTGTCTTAAAGAGAAACACCGGACATGCTACATACACAGCTT 6540
Db 6794 CTTGCAATTCCTGGAAGTGTCTTAAAGAGAAACACCGGACATGCTACATACACAGCTT 6853
QY 6541 CCATCTTCATTAATCTCTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA 6600
Db 6854 CCATCTTCATTAATCTCTCTGCGCAGGATATTCAGCATCTCTCCAGAGCAAAAAGCGA 6913
QY 6601 CTCACATAGAGACTACTCTCTCTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT 6660
Db 6914 CTCACATAGAGACTACTCTCTCTCTCAGACAACACTTGACCAAGTATTTGTGAACTTT 6973
QY 6661 GCGAAGGACCAAGTATGATGACACATTAAGAGCCTCTCATACACAAAACACGACA 6720
Db 6974 GCGAAGGACCAAGTATGATGACACATTAAGAGCCTCTCATACACAAAACACGACA 7033
QY 6721 GTAGTGGAGCTTGCACTCTCTCATCTCTCTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
Db 7034 GTAGTGGAGCTTGCACTCTCTCATCTCTCTCTACAGGATGAGAAAGTGAAGAAAGCTAT 7093
QY 6781 GTAT 6784
Db 7094 GTAT 7097
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RESULT 5

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US-09-984-827-105
; Sequence 105, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c o r g
US-09-984-827-105
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Query Match 99.7%; Score 6766.4; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6773; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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Db 314 ATGCTTTGTTGGCTCAGCTGAGTTGCTGCTGTGGGAAGAACCTTCACCTTTTCAAGAAGA 373
QY 61 CAAACATGTCAGCTGTTTACTGGAAGTGGCTGGCTCTATTTATTCCTGATCCTGATC 120
Db 374 CAAACATGTCAGCTGTTTACTGGAAGTGGCTGGCTCTATTTATTCCTGATCCTGATC 433
QY 121 TCTGTTGGCTGAGCTACCCACCTATGACACATGAATGCCATTTTCCAAATAAGCC 180
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Db 494 ATGCCCTCTGCAGGAACACATTCCTTGGTTCAGGGGATATCTGTAATGCAACAACCC 553
QY 241 TGTTCCTGTTACCCGACTCCTTGGGAGGCTCCCGAGGTGTGTGAAAATTTTAAACAATCC 300
Db 554 TGTTCCTGTTACCCGACTCCTTGGGAGGCTCCCGAGGTGTGTGAAAATTTTAAACAATCC 613
QY 301 ATTGTTGGCTCCGCTGTTCTCAGATGCTCGGAGGCTCTCTTTTATACAGCCAGAAAGACCC 360
Db 614 ATTGTTGGCTCCGCTGTTCTCAGATGCTCGGAGGCTCTCTTTTATACAGCCAGAAAGACCC 673
QY 361 AGCATGAAGGACATGCGCAAAAGTTCTGTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 420
Db 674 AGCATGAAGGACATGCGCAAAAGTTCTGTGAGAACATTACAGCAGATCAAGAAATCCAGTCA 733
QY 421 AACTTGAAGCTTCAAGATTTCTGTGTGACAAATGAAACCTTCTCTGSGTTCTTATATCAC 480
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QY 481 AACCTCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGTAGGGGCTGTGATCTCTTCCAC 540
Db 794 AACCTCTCTCTCCCAAGTCTACTGTGACAAAGATGCTGTAGGGGCTGTGATCTCTTCCAC 853
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Db 974 AAACCTGGCTGCAGAGCGAGTACTCTGTTCCAAACATGGACATCCTGAAGCAATCTCTG 1033
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QY 781 TTGCTGCATAGTCTTGGGACTCTGCCCCAGAGCTGTTTCAGCATGAGAGCTGGAGTGAC 840
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QY 841 ATGCGACAGAGGAGTGTATTTCTGACCAATGTGACAGCTCCAGCTCCCTCCCAAAATC 900
Db 1154 ATGCGACAGAGGAGTGTATTTCTGACCAATGTGACAGCTCCAGCTCCCTCCCAAAATC 1213
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QY 961 TCTCTCACTGGTATGAGGACAAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1020
Db 1274 TCTCTCACTGGTATGAGGACAAACTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG 1333
QY 1021 GAAGATGCTGAACCTTCTATGACAACTCTACAACCTCTTACTGCAATGATTTGATGAAG 1080
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QY 1141 GGAAGATCCTGTATACACTGACACTCCAGCCACAGCAGCTCATGCTGAGGTGAAC 1200
Db 1454 GGAAGATCCTGTATACACTGACACTCCAGCCACAGCAGCTCATGCTGAGGTGAAC 1513
QY 1201 AAGACCTTCCAGGAATGGCTGTGTTCCATGATCTGGAAGGCAATGTGGAGGAACCTCAGC 1260
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QY 1261 CCCAAGATCTGGACCTTCATATGGAGAACAGACCCAGAAATGGACCTTGTCCGGATGCTGTG 1320
DB 1574 CCCAAGATCTGGACCTTCATATGGAGAACAGACCCAGAAATGGACCTTGTCCGGATGCTGTG 1633
QY 1321 GACAGCAGGACATGACCACTTTTGGACACAGCAGTGGATGGCTTAGATTTGGACAGCC 1380
DB 1634 GACAGCAGGACATGACCACTTTTGGACACAGCAGTGGATGGCTTAGATTTGGACAGCC 1693
QY 1381 CAAGACATCGTGGCGTTTGGCCAAAGCACCAGAGAGATGTCAGTCCAGTAAATGGTTCT 1440
DB 1694 CAAGACATCGTGGCGTTTGGCCAAAGCACCAGAGAGATGTCAGTCCAGTAAATGGTTCT 1753
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DB 1754 GTGTACACCTGGAGAGAGCTTTCACGAGACTAACACAGCAATCCGGACCATATCTCGC 1813
QY 1501 TTCATGGAGTGTCTCAACCTGAAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1560
DB 1814 TTCATGGAGTGTCTCAACCTGAAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1873
QY 1561 AACAACTCCATGAGCTGCTGGATGAGAGAGTTCCTGGCGTGGTATTTGTTCACCTGGA 1620
DB 1874 AACAACTCCATGAGCTGCTGGATGAGAGAGTTCCTGGCGTGGTATTTGTTCACCTGGA 1933
QY 1621 ATTACTCCAGGAGCAGATTGAGTGGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1680
DB 1934 ATTACTCCAGGAGCAGATTGAGTGGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1993
QY 1681 GACATGTGGAGAGACAAATAAATCAAGATGGGTACTGGACCCCTGGTCTCGAGCT 1740
DB 1994 GACATGTGGAGAGACAAATAAATCAAGATGGGTACTGGACCCCTGGTCTCGAGCT 2053
QY 1741 GACCCCTTTGAGGACATGGGTACGTCCTGGGGGCTTCGCTACTTCAGAGATGGTG 1800
DB 2054 GACCCCTTTGAGGACATGGGTACGTCCTGGGGGCTTCGCTACTTCAGAGATGGTG 2113
QY 1801 GAGCAGGCAATCATAGGCTGTGACGGCCACCGAGAGAAACTGGTCTATATGCAA 1860
DB 2114 GAGCAGGCAATCATAGGCTGTGACGGCCACCGAGAGAAACTGGTCTATATGCAA 2173
QY 1861 CAGATGCCCTATCCCTGTACCTTGTATGACATCTTCTCGCGGTGATGACCGGTCAATG 1920
DB 2174 CAGATGCCCTATCCCTGTACCTTGTATGACATCTTCTCGCGGTGATGACCGGTCAATG 2233
QY 1921 CCCCTTTCATGACCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCTGT 1980
DB 2234 CCCCTTTCATGACCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCTGT 2293
QY 1981 TATGAGAGGAGGACGCTGAAAGAGACCATGCGGATCATGGGCTGGACACAGCAT 2040
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DB 2414 GTGGTCATCTCGAAGTATAGAAACCTGTGCCCTACAGTAGATCCAGCGTGGTTGTC 2473
QY 2161 TTCCCTGTCGCTGTGTGCTGGTACAACTCTGACAGTCTTCCCTGATAGACACTCTTC 2220
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QY 2461 CTCACCACTTCATCTCCATGATGCTGTTTGCACACTTCTCTCTATGGGTTGATGACCTGG 2520
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QY 2521 TACATTTGAGTGTCTTTCCAGGCGAGTACGGAATTTCCAGGCGCTGTTATTTTCCCTTGC 2580
DB 2834 TACATTTGAGTGTCTTTCCAGGCGAGTACGGAATTTCCAGGCGCTGTTATTTTCCCTTGC 2893
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DB 2894 ACCAAGTCTCTGTTTGGCGAGGAAGTGTATGAGAGAGCCACCTTGTTCACACAG 2953
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QY 3421 TCCTGCAGAAACAGTAGTACCTGTCTATACCTTGAAGAGGACAGTGTCTCTCAG 3480

Db	3734	TCCTGCAGAAACAGTAGTACACTGTGTATACCTGAAAGGAGGACAGTGTTCCTCAG	3793
Qy	3481	AGCAGTTCGTATGCTCGGCTGGGACGACCATGAGAGTGACAGCTGACCATCGATGTC	3540
Db	3794	AGCAGTTCGTATGCTCGGCTGGGACGACCATGAGAGTGACAGCTGACCATCGATGTC	3853
Qy	3541	TCCTGCTATCTCAAACCTCATCAGGAAGCATGTCTGAAGCCCGGCTGTGTGAAGACATA	3600
Db	3854	TCCTGCTATCTCAAACCTCATCAGGAAGCATGTCTGAAGCCCGGCTGTGTGAAGACATA	3913
Qy	3601	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGAGGCTTTGTGGAA	3660
Db	3914	GGGCATGAGCTGACCTATGTGCTGCCATGAAGCTGCTAAGGAGGAGGCTTTGTGGAA	3973
Qy	3661	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTTGGGCATTTCTAGTTATGGCATCTCA	3720
Db	3974	CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTTGGGCATTTCTAGTTATGGCATCTCA	4033
Qy	3721	GAGACGCCCTGGAAGAAATATTCCTCAAGTGGCCGAGAGAGTGGGTGGATGCTGAG	3780
Db	4034	GAGACGCCCTGGAAGAAATATTCCTCAAGTGGCCGAGAGAGTGGGTGGATGCTGAG	4093
Qy	3781	ACCTCAGATGGTACCTTGGCCAGACAGAAACAGCGGGGGCCITCGGGGACAAAGCAGAGC	3840
Db	4094	ACCTCAGATGGTACCTTGGCCAGACAGAAACAGCGGGGGCCITCGGGGACAAAGCAGAGC	4153
Qy	3841	TGCTTTGGCCCGTTCACCTGAAGATGATGCTGCTGATCCAAATGATCTGACATAGACCCA	3900
Db	4154	TGCTTTGGCCCGTTCACCTGAAGATGATGCTGCTGATCCAAATGATCTGACATAGACCCA	4213
Qy	3901	GAATCCAGAGAGACACACTTGTCTAGTGGATGGATGCAAGGGTCTCTACCAAGGTGAA	3960
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Qy	3961	GGCTGGAACCTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAGAGACTGCTAATGGC	4020
Db	4274	GGCTGGAACCTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAGAGACTGCTAATGGC	4333
Qy	4021	AGACGGAGTCGGAAGAGATTTTGTCTCAGATTGCTGCCAGCTGTGTTTGCTGCTGATT	4080
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Qy	4081	GCCCTTGTGTTCAGCCTGTATGCTGGCACCCCTTTGGCAAGTACCCCGACGCTGGAACTTCAG	4140
Db	4394	GCCCTTGTGTTCAGCCTGTATGCTGGCACCCCTTTGGCAAGTACCCCGACGCTGGAACTTCAG	4453
Qy	4141	CCCTGGATGTACACAGCAACAGTACATTTGTGTCAGATGCTGCCAGCTGTGTTTGCTGCTGATT	4200
Db	4454	CCCTGGATGTACACAGCAACAGTACATTTGTGTCAGATGCTGCCAGCTGTGTTTGCTGCTGATT	4513
Qy	4201	ACCTTGGAACTCTTAAACGCCCTTCACCAAGACCCCTGGCCTTCGGGACCCGCTGTATGGAA	4260
Db	4514	ACCTTGGAACTCTTAAAGGCCCTTCACCAAGACCCCTGGCCTTCGGGACCCGCTGTATGGAA	4573
Qy	4261	GGAACCCATCCAGACAGCCCTGCCAGGACGGGAGGAGAGTGGACCACTGGCCCCA	4320
Db	4574	GGAACCCATCCAGACAGCCCTGCCAGGACGGGAGGAGAGTGGACCACTGGCCCCA	4633
Qy	4321	GTTCGCCAGACCATCATGGACCTCTTCCAGATGGGAATGGGAATGGCAATGCGAACCCCTTCA	4380
Db	4634	GTTCGCCAGACCATCATGGACCTCTTCCAGATGGGAATGGGAATGGCAATGCGAACCCCTTCA	4693
Qy	4381	CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAGATGCTGCGCTGTGTGCCCCAGGG	4440
Db	4694	CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAGATGCTGCGCTGTGTGCCCCAGGG	4753
Qy	4441	GCAGGGGGCTGCCTCCTCCACAAAGAAACAAAACACTGCAGATATCTCTTCAGSACTG	4500
Db	4754	GCAGGGGGCTGCCTCCTCCACAAAGAAACAAAACACTGCAGATATCTCTTCAGSACTG	4813
Qy	4501	ACAGGAAGAAACATTTCCGATTATCTGTGAAGAGCTGTATGTCAGATCATAGCCAAAAGC	4560

Db	4814	ACAGGAAGAAACATTTCCGATATATCTGTTGAAGACGTATGTGCGAGATCATAGCCAAAGC	4873
QY	4561	TTAAAGAAACAAGATCTGGGTGAATCAGATTTAGCTATGCGCGCTTTTCCTCGGGTGTCAGT	4620
Db	4874	TTAAAGAAACAAGATCTGGGTGAATCAGATTTAGGTATGCGCGCTTTTCCTCGGGTGTCAGT	4933
QY	4621	AATATCTAAGCACTTCTCCGAGTCAAGAAGTTAATGATGCCATCAACAATAGAGAAA	4680
Db	4934	AATACTCAAGCACTTCTCCGAGTCAAGAAGTTAATGATGCCACCAACAATGAAGAAA	4993
QY	4681	CACCTAAAGCTGCCCAAGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	4740
Db	4994	CACCTAAAGCTGCCCAAGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	5053
QY	4741	ATGCAGGACTGGACACACAGAATAATGTCAAGGTGTGGTTCATAATAACAAGGCTGGCAT	4800
Db	5054	ATGCAGGACTGGACACACAGAATAATGTCAAGGTGTGGTTCATAATAACAAGGCTGGCAT	5113
QY	4801	GCAATCAGCTCTTCTCGTAATGTCAACAATGCCATCTCCGGGCCAACCTGCAAAAG	4866
Db	5114	GCAATCAGCTCTTCTCGTAATGTCAACAATGCCATCTCCGGGCCAACCTGCAAAAG	5173
QY	4861	GGAGAGAACCCTAGCCATPATGGAAATTAAGTGTCTTTCATATCCTCCCTGAATCTCACCAAG	4920
Db	5174	GGAGAGAACCCTAGCCATPATGGAAATTAAGTGTCTTTCATATCCTCCCTGAATCTCACCAAG	5233
QY	4921	CAGCAGCTCTCAGAGGTGCTCTGATGACCAATCAGTGGATGCTTGTGTGCCATCTGT	4980
Db	5234	CAGCAGCTCTCAGAGGTGCTCTGATGACCAATCAGTGGATGCTTGTGTGCCATCTGT	5293
QY	4981	GTCACTTTTGCAATGCTTCTGCCAGCCAGCTTTGTGTATTCCTGATCCAGAGCGG	5040
Db	5294	GTCACTTTTGCAATGCTTCTGCCAGCCAGCTTTGTGTATTCCTGATCCAGAGCGG	5353
QY	5041	GTCCAGCAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCACTTACTGGCTC	5100
Db	5354	GTCCAGCAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCACTTACTGGCTC	5413
QY	5101	TCTAATTTTGTCTGGGATATGCAATTAAGTTGTCCTTCCCTGCCACACTGTGTCATATCATC	5160
Db	5414	TCTAATTTTGTCTGGGATATGCAATTAAGTTGTCCTTCCCTGCCACACTGTGTCATATCATC	5473
QY	5161	TTCACTCGTTTCAGCAGAAAGTCTATGTGCTCCACCAATCTGCCTGTGTAGCCCTT	5220
Db	5474	TTCACTCGTTTCAGCAGAAAGTCTATGTGCTCCACCAATCTGCCTGTGTAGCCCTT	5533
QY	5221	CTACTTTTGTGTATGGGTGGTCAATCACACCTCTCATATCCAGCCCTCTTGTGTCTC	5280
Db	5534	CTACTTTTGTGTATGGGTGGTCAATCACACCTCTCATATCCAGCCCTCTTGTGTCTC	5593
QY	5281	AAGATCCGACACACGCTATGTGTGTCTACAGCGTGAACCTCTTCAATTGGCATTAAT	5340
Db	5594	AAGATCCGACACACGCTATGTGTGTCTACAGCGTGAACCTCTTCAATTGGCATTAAT	5653
QY	5341	GGCAGCGTGGCCACCTTTTGTCTGGAGCTGTTCAACCGCAATAAGCTGAATAATATCAAT	5400
Db	5654	GGCAGCGTGGCCACCTTTTGTCTGGAGCTGTTCAACCGCAATAAGCTGAATAATATCAAT	5713
QY	5401	GATATCCTGAAGTCCGTGTTCTTGATCTTCCCAATATTTTGGCTGGGACAGGCTCATC	5460
Db	5714	GATATCCTGAAGTCCGTGTTCTTGATCTTCCCAATATTTTGGCTGGGACAGGCTCATC	5773
QY	5461	GACATGGTGAAGAACACAGCAATGGCTGATGCCCTGGAAAGGTTTGGGAGATCCCTTT	5520
Db	5774	GACATGGTGAAGAACACAGCAATGGCTGATGCCCTGGAAAGGTTTGGGAGATCCCTTT	5833
QY	5521	GTGTCAACATTAATCTTTGGGACTTTGGTGGGACGAAACCTCTTCCCATGCGCGTGAAGG	5580
Db	5834	GTGTCAACATTAATCTTTGGGACTTTGGTGGGACGAAACCTCTTCCCATGCGCGTGAAGG	5893
QY	5581	GTGGTGTCTTCTCAATTAATCTTCTGATCCAGTACAGATTTCTTATCATGAGCCCAACCT	5640
Db	5894	GTGGTGTCTTCTCAATTAATCTTCTGATCCAGTACAGATTTCTTATCATGAGCCCAACCT	5953

Db 2765 ACCAAGTCTACTGGTTGGCGAGGAAAGTATGAGAAGAGCACCCCTGGTTCCAAACCAG 2824
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Db 2825 AAGAGAAATATCAGAAATCTGCATGGAGAGGAAACCCACCACCTTGAAGCTGGCGGTGTC 2884
QY 2701 ATTGAGAACCTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCCTGGGA 2760
Db 2885 ATTGAGAACCTGGTAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCCTGGGA 2944
QY 2761 CTGAATTTTATGAGGCCAGATCACTCTCTCTGGCCACAAATGAGGGGGAAGAGC 2820
Db 2945 CTGAATTTTATGAGGCCAGATCACTCTCTCTGGCCACAAATGAGGGGGAAGAGC 3004
QY 2821 ACCACCATGTCATCTGACCGGGTTGTTCCTCCCGACCTCGGGCACCCCTACATCCTG 2880
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QY 2881 GGAAGAGACATTCGCTCTGAGATGAGCACCATCCGCGAGACCTGGGGCTGTCCCCAG 2940
Db 3065 GGAAGAGACATTCGCTCTGAGATGAGCACCATCCGCGAGACCTGGGGCTGTCCCCAG 3124
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Db 3185 AAAGGCTCTCTGAGAGCAGTGAAGCGGAGATGAGCAGATGCCCTGATGTTGT 3244
QY 3061 TTGCCATCAAGCAAGCTGAAAACAAACAGCCAGCTGTGAGTGAATGAGAGAAAG 3120
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QY 3121 CTATCTGTGGCTTGGCTTGTTCGGGGATCTAAGTGTCTATCTGATGAACCCACA 3180
Db 3305 CTATCTGTGGCTTGGCTTGTTCGGGGATCTAAGTGTCTATCTGATGAACCCACA 3364
QY 3181 GCTGTGTGAGACCTTACTCCCGAGGGAATATGGAGCTGCTGCTGAATACCGACA 3240
Db 3365 GCTGTGTGAGACCTTACTCCCGAGGGAATATGGAGCTGCTGCTGAATACCGACA 3424
QY 3241 GGGCCACCATATCTCTCTACACACACATGATGAAGCGGAGCTCGTGGGGACAGG 3300
Db 3425 GGGCCACCATATCTCTCTACACACACATGATGAAGCGGAGCTCGTGGGGACAGG 3484
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Db 3485 ATTGCCATCATCTCCATGGGAAGCTGTGCTGTGGCTCTCCCTGTTTCTGAAGAC 3544
QY 3361 CAGCTGGGAACAGGCTACTACCTGACCTTGTGTCAGAAAGATGTGGAATCTCCCTCAGT 3420
Db 3545 CAGCTGGGAACAGGCTACTACCTGACCTTGTGTCAGAAAGATGTGGAATCTCCCTCAGT 3604
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Db 3605 TCTCTGAGAAACAGTAGTAGCCTGTGTCATACCTCAAAAGAGGAGACAGTGTCTCTAG 3664
QY 3481 AGCAGTCTGTGCTGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3540
Db 3665 AGCAGTCTGTGCTGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3724
QY 3541 TCTGCTATCTCAACCTCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3600
Db 3725 TCTGCTATCTCAACCTCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3784
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Db 3845 CTCCTTTCATGAGATGACCGGCTCTCAGACCTGGGCAATTTCTAGTATGGCATCTCA 3904

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QY 3781 ACCTCAGATGTTACCTTGGCCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3840
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Db 4085 GAATCCAGAGACAGACCTTCTCAGTGGATGGATGCAAAAGGTCTTACAGGTGAAA 4144
QY 3961 GCTGGAAACTTACACAGAACAGTCTTGGCCCTTTTGTGGAGAGAGAGTGTCTAATTGCC 4020
Db 4145 GCTGGAAACTTACACAGAACAGTCTTGGCCCTTTTGTGGAGAGAGAGTGTCTAATTGCC 4204
QY 4021 AGACGAGCTCGAAAGGATTTTGTCTCAGATTTGTCTGCCAGCTGTCTTGTCTGCATT 4080
Db 4205 AGACGAGCTCGAAAGGATTTTGTCTCAGATTTGTCTGCCAGCTGTCTTGTCTGCATT 4264
QY 4081 GCCCTTGTGTTAGCCTGATCGTGGCCCTTTTGGCAAGTACCCAGCTGGAACTTCAG 4140
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QY 4141 CCCTGGATGTAAAGAACAGTACACATTTCTCAGCAATGATCTCTGAGGACACCGGA 4200
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QY 4201 ACCCTGGAACTTTAAAGCCCTTACCAGAACCTTGGCTTGGGAGCCGCTGTATGAA 4260
Db 4385 ACCCTGGAACTTTAAAGCCCTTACCAGAACCTTGGCTTGGGAGCCGCTGTATGAA 4444
QY 4261 GGAACCCATCCAGACACGCCCTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4320
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Db 4625 GCAGGGGGCTGCTCTCCAGAAAGAAACAAACACTGCAGATATCCCTTCAGGACCTG 4684
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Db 4685 ACAGGAAGAAACATTTCCGATTTCTGGTGAAGACGATGTCAGATCATAGCCAAAGC 4744
QY 4561 TTAAGAAACAGATCTGGTGAATGATTTAGGTATGGCGCTTTCCCTGGGTGTCAGT 4620
Db 4745 TTAAGAAACAGATCTGGTGAATGATTTAGGTATGGCGCTTTCCCTGGGTGTCAGT 4804
QY 4621 AATACTCAAGACCTTCTCCGAGTCAAGAGTAAATGATGCCACCAACAAATGAAGAA 4680
Db 4805 AATACTCAAGACCTTCTCCGAGTCAAGAGTAAATGATGCCACCAACAAATGAAGAA 4864
QY 4681 CACTTAAGCTGCCAGGACAGTCTGTCAGATTCGATTTCTCAACAGCTTGGAGAGTTT 4740
Db 4865 CACTTAAGCTGCCAGGACAGTCTGTCAGATTCGATTTCTCAACAGCTTGGAGAGTTT 4924
QY 4741 ATGACAGGACTGGACACCCAGAAATAATGTCAAGGTGTGGTTCAATAACAGGCTGGCAT 4800
Db 4925 ATGACAGGACTGGACACCCAGAAATAATGTCAAGGTGTGGTTCAATAACAGGCTGGCAT 4984

QY	4801	GCAATCAGCTCTTCTCTGAAATGTCATCAACAATGCCATTCCTCCGGCCCAACCTGCTCRAAG	4866
Db	4985	GCAATCAGCTCTTCTCTGAAATGTCATCAACAATGCCATTCCTCCGGCCCAACCTGCTCRAAG	5044
QY	4861	GGAGAAACCCTAGCCATTATGGAATTACTGTTTCAATCATCCCTGGAATCTCACCAAG	4920
Db	5045	GGAGAAACCCTAGCCATTATGGAATTACTGTTTCAATCATCCCTGGAATCTCACCAAG	5104
QY	4921	CACGAGCTCTCAGAGGTGGCTCTGATGATCCACATCAGTGGATGTCCTTGTGTCATCTGT	4980
Db	5105	CACGAGCTCTCAGAGGTGGCTCCGATGACCAATCAGTGGATGTCCTTGTGTCATCTGT	5164
QY	4981	GTCACTCTTTGCAATGTCCTGCCAGCAGCTTGTGCTATCTCTGATCCAGAGCGG	5040
Db	5165	GTCACTCTTTGCAATGTCCTGCCAGCAGCTTGTGCTATCTCTGATCCAGAGCGG	5224
QY	5041	GTCAGAAAGCAAAACACCTCGAGTTCATCAGTGAGGTGAAGCCTGTCATCTACTGGCTC	5100
Db	5225	GTCAGAAAGCAAAACACCTCGAGTTCATCAGTGAGGTGAAGCCTGTCATCTACTGGCTC	5284
QY	5101	TCATAATTTGCTCGGATATGTGCAATACGTTGTCCTGCCACATGGTCATTAATCATC	5160
Db	5285	TCATAATTTGCTCGGATATGTGCAATACGTTGTCCTGCCACATGGTCATTAATCATC	5344
QY	5161	TTCACTCTGCTCCAGCAGAAGTCCTATGTGTCCTCCACCAATCTGCCCTGTCAGCCCTT	5220
Db	5345	TTCACTCTGCTCCAGCAGAAGTCCTATGTGTCCTCCACCAATCTGCCCTGTCAGCCCTT	5404
QY	5221	CTACTTTTGTGATGGGTGGTCAATCACACCTCTCATGTACCCAGAGCTCCTTGTGTTC	5280
Db	5405	CTACTTTTGTGATGGGTGGTCAATCACACCTCTCATGTACCCAGAGCTCCTTGTGTTC	5464
QY	5281	AAGATCCCAAGCAGACGCTATGTGTGTCACACGAGTGAACCTCTTCATTGGCATTAAT	5340
Db	5465	AAGATCCCAAGCAGACGCTATGTGTGTCACACGAGTGAACCTCTTCATTGGCATTAAT	5524
QY	5341	GGCAGGCTGCCACCTTTGTGTGAGCTGTTCCACCGACAATAAGCTGAATAATATCAAT	5400
Db	5525	GGCAGGCTGCCACCTTTGTGTGAGCTGTTCCACCGACAATAAGCTGAATAATATCAAT	5584
QY	5401	GATATCTGAAAGTCGCTGTTCTTGATCTTCCACATTTTTGCTGGGACGAGGCTCATC	5460
Db	5585	GATATCTGAAAGTCGCTGTTCTTGATCTTCCACATTTTTGCTGGGACGAGGCTCATC	5644
QY	5461	GACATGTTAAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAAATCGCTTT	5520
Db	5645	GACATGTTAAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAAATCGCTTT	5704
QY	5521	GTGTCACCAATATCTTTGGACATGTGGGACAAACCTCTTCGCCATGGCCGTGGAGGG	5580
Db	5705	GTGTCACCAATATCTTTGGACATGTGGGACAAACCTCTTCGCCATGGCCGTGGAGGG	5764
QY	5581	GTGGTGTCTTCCTCATTAATCTGTGATGCCAGTACAGATCTTCATCAGGCCACGACCT	5640
Db	5765	GTGGTGTCTTCCTCATTAATCTGTGATGCCAGTACAGATCTTCATCAGGCCACGACCT	5824
QY	5641	GTAATGCAAAAGTATCTCCTCTGATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5700
Db	5825	GTAATGCAAAAGTATCTCCTCTGATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5884
QY	5701	AGAATCTTGATGGTGGAGCCAGATGACATCTTTAGAAATCAAGGAGTTCACGAAAGATA	5760
Db	5885	AGAATCTTGATGGTGGAGCCAGATGACATCTTTAGAAATCAAGGAGTTCACGAAAGATA	5944
QY	5761	TATAGAGGAAGCGGAAGCCTGCTGTGACAGGATTTGCGTGGGCAATTCCTCCTGGTGAG	5820
Db	5945	TATAGAGGAAGCGGAAGCCTGCTGTGACAGGATTTGCGTGGGCAATTCCTCCTGGTGAG	6004
QY	5821	TGCTTTGGGCTCTCGGAGTTAATGGGCTGGAAATCATCAACTTCAAGATCTTAACA	5880
Db	6005	TGCTTTGGGCTCTCGGAGTTAATGGGCTGGAAATCATCAACTTCAAGATCTTAACA	6064
QY	5881	GGAGATACCACCTGTTACCAGAGAGATGCTTTCCCTTAACAAAAATAGTATCTTATCAAC	5940

Db	6065	GGAGATACCAGTGTACAGAGAGAGATGCTTTCCTTTACACAAATAGTAATCTTATCAAC	6124
QY	5941	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTCGTGATGCCATCAGAGCTG	6000
Db	6125	ATGCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTCGTGATGCCATCAGAGCTG	6184
QY	6001	TTGACTGGGAGAGAACACGTGGAGTTCCTTTGGCCCTTTTGGAGAGAGTCCACAGAGAAAGAA	6060
Db	6185	TTGACTGGGAGAGAACACGTGGAGTTCCTTTGGCCCTTTTGGAGAGAGTCCACAGAGAAAGAA	6244
QY	6061	GTGGCAAGTGTGGTGAGTGGGCGATTCGGAAATCGGCCCTCCTCAAGTATGGAAGAAAA	6120
Db	6245	GTGGCAAGTGTGGTGAGTGGGCGATTCGGAAATCGGCCCTCCTCAAGTATGGAAGAAAA	6304
QY	6121	TATGCTGTAACTATAGTGGAGSCAACAAACGAAGCTCTCTACAGCATTGGCTTTGATC	6180
Db	6305	TATGCTGTAACTATAGTGGAGSCAACAAACGAAGCTCTCTACAGCATTGGCTTTGATC	6364
QY	6181	GGGGGGGCTCCTGTGTGTTCCTGGATGAACCCACACAGGATGGATCCCAAGACCCCGG	6240
Db	6365	GGGGGGGCTCCTGTGTGTTCCTGGATGAACCCACACAGGATGGATCCCAAGACCCCGG	6424
QY	6241	CGGTTCTGTGGAAATGTGCCCTTAAGTGTGTGTCAGGAGGGAGATCAGTAGTCTTAC	6300
Db	6425	CGGTTCTGTGGAAATGTGCCCTTAAGTGTGTGTCAGGAGGGAGATCAGTAGTCTTAC	6484
QY	6301	TCTCATAGTATGGAAGAAATGTGAAGCTCTTTGCATCTAGGATGGCAATCATGGTCAATGGA	6360
Db	6485	TCTCATAGTATGGAAGAAATGTGAAGCTCTTTGCATCTAGGATGGCAATCATGGTCAATGGA	6544
QY	6361	AGGTTTCAGGTGCCCTTGGCAGTGTCCAGCATCTAAAAATAGGTTTGGAGATGGTTATACA	6420
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QY	6421	ATAGTTGTACGAATAGCAGGGTCCAAACCCGACCTGAAAGCCTGTCCAGGATTTCTTTGGA	6480
Db	6605	ATAGTTGTACGAATAGCAGGGTCCAAACCCGACCTGAAAGCCTGTCCAGGATTTCTTTGGA	6664
QY	6481	CTTCGATTTCTCGGAAGTGTCTTAAAGAGAAACACCCGAAACATGCTACAATACCAGCTT	6540
Db	6665	CTTCGATTTCTCGGAAGTGTCTTAAAGAGAAACACCCGAAACATGCTACAATACCAGCTT	6724
QY	6541	CCATCTTCATATATCTTCTCTGGCCAGGATATTCAGATCTCTCTCCAGAGCAAAAGCGA	6600
Db	6725	CCATCTTCATATATCTTCTCTGGCCAGGATATTCAGATCTCTCTCCAGAGCAAAAGCGA	6784
QY	6601	CTCCACATAGAAGACTACTCTGTTTCTCAGACCAACATTGACCAAGTATTTGTGAATTT	6660
Db	6785	CTCCACATAGAAGACTACTCTGTTTCTCAGACCAACATTGACCAAGTATTTGTGAATTT	6844
QY	6661	GCCAAAGCAAGTAGTATGATGACCACTTTAAAGACCTCTCATTTACACAAAAACGAGACA	6720
Db	6845	GCCAAAGCAAGTAGTATGATGACCACTTTAAAGACCTCTCATTTACACAAAAACGAGACA	6904
QY	6721	GTAGTGGACGTTGCAGTTCCTCACATCTTTCTACAGGATGAGAAAGTCAAAAGAAAGTAT	6780
Db	6905	GTAGTGGACGTTGCAGTTCCTCACATCTTTCTACAGGATGAGAAAGTCAAAAGAAAGTAT	6964
QY	6781	GTAT 6784	
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RESULT 7
US-03-984-827-92
; Sequence 92, Application US/09984827
; Publication No. US20030036234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFLS, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS

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; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; METHOD OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
; IS-09-984-827-92

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Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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361	AGCATGAAGGACATCGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAATCCAGTGCA	420
674	AGCATGAAGGACATCGCAAAAGTTCTGAGAACATTACAGCAGATCAAGAATCCAGTGCA	733
421	AACTTGAAGCTTCAAGATTTCCTGGTGGACAATGAACACTTCTCTGGTTCCTATATCAC	480
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854	AAGGTATTTTTGCAAGGCTACAGTTTACATTGTGACAAGTCTGTGCATTGGATCAAAATCA	913
601	GAAGAGATGATTCAACTTTGGTGACCAAGAAGTTTCTGAGCTTTCTGGCCTACCAAAAGGAG	660
914	GAAGAGATGATTCAACTTTGGTGACCAAGAAGTTTCTGAGCTTTCTGGCCTACCAAGGAG	973
661	AAACTGGCTGCAGACGCGAGTACTTCGTTTCCAACTGGACATCTCTGAAGCCAAATCCTG	720
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QY 1801 GAGAGGCAATCATCAGGGTGTGACGGGACCGAGAGAAACCTGGTGTCTATATGCAA 1860
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Db 2114 GAGCAGGCAATCATCAGGGTGTGACGGGACCGAGAGAAACCTGGTGTCTATATGCAA 2173
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QY 1861 CAGATGCCATATCCCTGTATACGTTGATGACATCTTCTGCGGTGATCAGCGCGTCAATG 1920
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Db 2174 CAGATGCCATATCCCTGTATACGTTGATGACATCTTCTGCGGTGATCAGCGCGTCAATG 2233
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QY 1921 CCCCTCTTCATGACGCTGGCCCTGGATTACTACAGTGGGTGTGATCATCAAGGGCATCGT 1980
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RESULT 8
US-09-984-827-93
; Sequence 93, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEUFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REUGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984,827
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/254,108
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; PRIOR APPLICATION NUMBER: FR 00/14037
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)

OTHER INFORMATION: a, t, c or g
US-09-984-827-93
Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db 1814 TTCATGGAGTGTCAACCTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC 1873
QY 1561 ACAAGTCCATGGAGTGTGGATGAGAGGAAGTTCTGGCTGATGTTGTTCACTGGA 1620
Db 1874 ACAAGTCCATGGAGTGTGGATGAGAGGAAGTTCTGGCTGATGTTGTTCACTGGA 1933
QY 1621 ATTACTCCAGGAGGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1934 ATTACTCCAGGAGGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1993
QY 1681 GACAAATGTGGAGAGCAAAATAAATCAAGGATGGGTACTGGACCCCTGGCTCGAGCT 1740
Db 1994 GACAAATGTGGAGAGCAAAATAAATCAAGGATGGGTACTGGACCCCTGGCTCGAGCT 2053
QY 1741 GACCCCTTTGAGGACATGGGTACGCTCTGGGGGCTTCCGCTACTTCCAGGATGTTGGT 1800
Db 2054 GACCCCTTTGAGGACATGGGTACGCTCTGGGGGCTTCCGCTACTTCCAGGATGTTGGT 2113
QY 1801 GAGCAGGAATCATCAGGCTGTGACGGGCAACCGAGAAAGAACTGGTGTCTATATGCAA 1860
Db 2114 GAGCAGGAATCATCAGGCTGTGACGGGCAACCGAGAAAGAACTGGTGTCTATATGCAA 2173
QY 1861 CAGATGCCCTATCCCTGTTAGTGTGATGACATCTTTTCGGGGTGTATGAGCCGCTCAATG 1920
Db 2174 CAGATGCCCTATCCCTGTTAGTGTGATGACATCTTTTCGGGGTGTATGAGCCGCTCAATG 2233
QY 1921 CCCCTCTTCATGACCTGGCTGGATTTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 1980
Db 2234 CCCCTCTTCATGACCTGGCTGGATTTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 2293
QY 1981 TATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGCCCTGGACACAGCATA 2040
Db 2294 TATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGCCCTGGACACAGCATA 2353
QY 2041 CTCCTGTTTGTGCTGATGAGCTCATCTCTCTCTTGTGAGCGTGGCTGCTGCTA 2100
Db 2354 CTCCTGTTTGTGCTGATGAGCTCATCTCTCTCTTGTGAGCGCTGGCTGCTA 2413

QY 2101 GTGGTCATCCTGAAGTATAGGAAACCTGCTGCCTACAGTATCCACGCTGCTGTTGTC 2160
Db 2414 GTGGTCATCCTGAAGTATAGGAAACCTGCTGCCTACAGTATCCACGCTGCTGTTGTC 2473
QY 2161 TTCCTGTCCGTTTGTGCTGTGGTGAACATCTCTGAGTCTTCCCTGATPAGACACTCTTC 2220
Db 2474 TTCCTGTCCGTTTGTGCTGTGGTGAACATCTCTGAGTCTTCCCTGATPAGACACTCTTC 2533
QY 2221 TCCAGAGCAACCTGGCAGCAGCCTGTGGGCACTACTACTTCAAGCTTACGCTTACCTGCCC 2280
Db 2534 TCCAGAGCAACCTGGCAGCAGCCTGTGGGCACTACTACTTCAAGCTTACGCTTACCTGCCC 2593
QY 2281 TACGTCCTGTGTGGTGGCATGGCAGACTACGTGGGCTTTCACACTCAAGATCTTCGCTAGC 2340
Db 2594 TACGTCCTGTGTGGTGGCATGGCAGACTACGTGGGCTTTCACACTCAAGATCTTCGCTAGC 2653
QY 2341 CTGCTGTCTCTCTGCTGCTTGGGTTTGGCTGTGAGTACTTTCGCTTTCGCTTTCGCTAGC 2400
Db 2654 CTGCTGTCTCTCTGCTGCTTGGGTTTGGCTGTGAGTACTTTCGCTTTCGCTTTCGCTAGC 2713
QY 2401 GGCATTGGAGTGCAGTGGGCAACCTGTTGAGAGTCTGTGGAGGAGATGGCTTCAAT 2460
Db 2714 GGCATTGGAGTGCAGTGGGCAACCTGTTGAGAGTCTGTGGAGGAGATGGCTTCAAT 2773
QY 2461 CTCACCACCTTCGATCTCGATGATGCTGTTGACACTTTCCTCTATGGGTTGATGACCTGG 2520
Db 2774 CTCACCACCTTCGATCTCGATGATGCTGTTGACACTTTCCTCTATGGGTTGATGACCTGG 2833
QY 2521 TACATTGAGGCTGTCTTCCAGGCACTAGCGAATTCCTAGGCTTTCCTGTTTCCTGTC 2580
Db 2834 TACATTGAGGCTGTCTTCCAGGCACTAGCGAATTCCTAGGCTTTCCTGTTTCCTGTC 2893
QY 2581 ACCAAGTCTTACTGTTGGGAGGAAGTATGAGAGAGCAACCTGTTTCCACACAG 2640
Db 2894 ACCAAGTCTTACTGTTGGGAGGAAGTATGAGAGAGCAACCTGTTTCCACACAG 2953
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Db 2954 AAGAGATGTCAGAAATCTCATGGAGGAGAACCCACCTTGAAGCTGCTGATGCTGCTG 3013
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Db 3014 ATTCAAGCTGTGTAAGTCTACCGAGATGGGATGAAGTGGCTGTGCTGATGCTGCTG 3073
QY 2761 CTGAATTTTATGAGGCCAGATCACTCTCTCTGAGTGGATGAAGTGGCTGTGCTGATGCTG 2820
Db 3074 CTGAATTTTATGAGGCCAGATCACTCTCTCTGAGTGGATGAAGTGGCTGTGCTGATGCTG 3133
QY 2821 ACCACCATGCTGTTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2880
Db 3134 ACCACCATGCTGTTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3193
QY 2881 GGAAGAGACATTCGCTGTGAGTGAACCATCCGGCAGAACCTGGGGTCTGCTGCTGCTG 2940
Db 3194 GGAAGAGACATTCGCTGTGAGTGAACCATCCGGCAGAACCTGGGGTCTGCTGCTGCTG 3253
QY 2941 CATTAACCTGCTGTTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
Db 3254 CATTAACCTGCTGTTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3313
QY 3001 AAGGGCTCTCTCAGAGACAGCTGAAGGGGAGATGGAGAGATGGCCCTGGATGTTGCT 3060
Db 3314 AAGGGCTCTCTCAGAGACAGCTGAAGGGGAGATGGAGAGATGGCCCTGGATGTTGCT 3373
QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGAGTGGATGAGAGAGAG 3120
Db 3374 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGAGTGGATGAGAGAGAG 3433
QY 3121 CTATCTGTGGCTTGGCTTGTGCGGGGATCTAAGGTTGTGATTTGATGAACCCACA 3180
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 QY 5401 GATATCTCAAGTCCGCTGTTCTGATCTCCACATTTTTGGCTGGAGAGGGCTCATC 5460
 Db 5714 GATATCTCAAGTCCGCTGTTCTGATCTCCACATTTTTGGCTGGAGAGGGCTCATC 5773
 QY 5461 GACATGGTGAAGAACACAGCAATGGCTGATGCCGTGGAAGTTTGGGGAGAGTCCGCTTT 5520
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 Db 5894 GTGGTGTCTTCTCTCAATTAATCTCTGATCCAGTACAGATTTCTCATCAGGCCAGACCT 5953
 QY 5641 GTAATGCAAGCTATCTCTCTGATGATGAAGTGAAGTGTGAGCGGGAAGACAG 5700
 Db 5954 GTAATGCAAGCTATCTCTCTGATGATGAAGTGAAGTGTGAGCGGGAAGACAG 6013
 QY 5701 AGAATCTTGTGTGGAGCCAGATGACATCTTAGAATCAAGGAGTTGACGAGATA 5760
 Db 6014 AGAATCTTGTGTGGAGCCAGATGACATCTTAGAATCAAGGAGTTGACGAGATA 6073
 QY 5761 TATAGAAGAACGGGAAGCTCTGTTGACAGGATTTGGGTGGGATTCCTCTCTGGTGA 5820
 Db 6074 TATAGAAGAACGGGAAGCTCTGTTGACAGGATTTGGGTGGGATTCCTCTCTGGTGA 6133
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 Db 6134 TGCTTTGGGCTCTCTGGAGTTAATGGGCTGGAATATCAACTTCAAGATGTTAACA 6193
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 Db 6194 GGAGTACCACCTGTACAGAGAGATGCTTCTTCAACAAAATAGTATCTTATCAAC 6253
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 Db 6254 ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGGTCCATCAGAGCTG 6313
 QY 6001 TTGACTGGGAGAGAACCTGGAGTTCTTTGGCTTTTGGAGAGGATGCCAGAGAA 6060
 Db 6314 TTGACTGGGAGAGAACCTGGAGTTCTTTGGCTTTTGGAGAGGATGCCAGAGAA 6373
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 Db 6374 GTTGGCAAGTGTGGTGGAGTGGGATCGGAACCTGGGCTCGTGAAGTATGGAGAAA 6433
 QY 6121 TATGCTGGTAACATATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGCCTTTGATC 6180
 Db 6434 TATGCTGGTAACATATAGTGGAGGCAACAAACCAAGCTCTCTACAGCCATGCCTTTGATC 6493
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 Db 6494 GCGGGCCCTCTGCTGGTGTCTTGGATGAACCCACAGGATGGATCCCAAGGCCGG 6553
 QY 6241 CGGTTCTTGTGAATTTGCCCTTAAGTGTGTCAGAGGGGAGATCAGTAGTGTTCATA 6300
 Db 6554 CGGTTCTTGTGAATTTGCCCTTAAGTGTGTCAGAGGGGAGATCAGTAGTGTTCATA 6613
 QY 6301 TCTCATAGTATGGAAGATGTAAGCTCTTTCACACTAGATGGCAATCATGTCAATGGA 6360
 Db 6614 TCTCATAGTATGGAAGATGTAAGCTCTTTCACACTAGATGGCAATCATGTCAATGGA 6673
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 Db 6734 ATAGTTGTACGAATAGCAGGGTCCAAACCGGACCTGGAAGCTGTCCAGATTTCTTGA 6793

QY 6481 CTTGCAATTTCTGGAGTGTGTTCTAAAAGAGAAACACCGGAACATGCTACATACAGCTT 6540
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 QY 6541 CCACTCTCATTTATCTCTCTGGCCAGGATATTCAGATTCCTCTCCAGAGCAAAAGCGA 6600
 Db 6854 CCACTCTCATTTATCTCTCTGGCCAGGATATTCAGATTCCTCTCCAGAGCAAAAGCGA 6913
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 QY 6661 GCCAAGACCACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 6720
 Db 6974 GCCAAGACCACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 7033
 QY 6721 GTAGTGACGTTGAGTCTTCACATCTTTCTACAGGATGAGAAGTGAAGAAGCTAT 6780
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 Db 7094 GTAT 7097

RESULT 9
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 ; Sequence 94, Application US/09984827
 ; Publication No. US20030056234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DENEFE, PATRICE
 ; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
 ; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
 ; APPLICANT: DUVERGER, NICOLAS
 ; APPLICANT: CAMBIEN, FRANCOIS
 ; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, AND
 ; FILE REFERENCE: 03806.0522-00000
 ; CURRENT APPLICATION NUMBER: US/09/984, 827
 ; PRIOR FILING DATE: 2002-04-01
 ; PRIOR APPLICATION NUMBER: 60/254,108
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: FR 00/14037
 ; PRIOR FILING DATE: 2000-10-31
 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 94
 ; LENGTH: 9870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (7138)
 ; OTHER INFORMATION: a, t, c or g
 US-09-984-827-94

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
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 Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGCTTGTGGCTCAGCTGAGGTTGCTGCTGTGGAGAACCTCACTTTTCAGAGAGA 60
 Db 314 ATGCTTGTGGCTCAGCTGAGGTTGCTGCTGTGGAGAACCTCACTTTTCAGAGAGA 373
 QY 61 CAACATGTCTCAGCTGTTACTGGAAGTGGCCTGCTCTATTATCTTCCTGATCCTGATC 120
 Db 374 CAACATGTCTCAGCTGTTACTGGAAGTGGCCTGCTCTATTATCTTCCTGATCCTGATC 433
 QY 121 TCTGTTGGCTGAGCTACCCACCCTATGACACACATGAATGCCATTTTCCAAATAAGCC 180
 Db 434 TCTGTTGGCTGAGCTACCCACCCTATGACACACATGAATGCCATTTTCCAAATAAGCC 493

Qy	181	ATGCCCTCTCAGAGAACTTCTCTTGGGTTTCAGGGATTATCTGTAAATGCCAACACCCC	240
Db	494	ATGCCCTCTCAGAGAACTTCTCTTGGGTTTCAGGGATTATCTGTAAATGCCAACACCCC	553
Qy	241	TGTTTCGGTTACCCGACTCCTCGGAGGCTCCCGAGTTGTGGAACTTTAACAAATCC	300
Db	554	TGTTTCGGTTACCCGACTCCTCGGAGGCTCCCGAGTTGTGGAACTTTAACAAATCC	613
Qy	301	ATTGTGGCTCCCTGTCTTCAGATGCTCGGAGGCTCTTTTATACGCCAGAAAGACACC	360
Db	614	ATTGTGGCTCCCTGTCTTCAGATGCTCGGAGGCTCTTTTATACGCCAGAAAGACACC	673
Qy	361	AGCATGAAGACATCGCAAAAGTTCTGACAACTTACAGCAGATCAAGAAATCCAGTCA	420
Db	674	AGCATGAAGACATCGCAAAAGTTCTGACAACTTACAGCAGATCAAGAAATCCAGTCA	733
Qy	421	AACCTGAAGCTTCAAGATTTCCTGTGGACATGAACCTTCTCTGGGTCTCTATATCAC	480
Db	734	AACCTGAAGCTTCAAGATTTCCTGTGGACATGAACCTTCTCTGGGTCTCTGTATCAC	793
Qy	481	AACCTCTCTCTCCAAAGTCTACTGTGGACAGATGCTGAGGGTGATGTCAATCTCCAC	540
Db	794	AACCTCTCTCTCCAAAGTCTACTGTGGACAGATGCTGAGGGTGATGTCAATCTCCAC	853
Qy	541	AAGTATTTTTGCAAGGCTACAGTTACATTTTGACAAGTCTGTGCAATGGATCAAAATCA	600
Db	854	AAGTATTTTTGCAAGGCTACAGTTACATTTTGACAAGTCTGTGCAATGGATCAAAATCA	913
Qy	601	GAAGAGATGATCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTTACCAAGGAG	660
Db	914	GAAGAGATGATCAACTTGGTGACCAAGAAGTTTCTGAGCTTTGTGGCTTACCAAGGAG	973
Qy	661	AAACTGGCTGCACAGAGGATCTCGTTCCACATGGACATCCCTGAAGCCATCTCTG	720
Db	974	AAACTGGCTGCACAGAGGATCTCGTTCCACATGGACATCCCTGAAGCCATCTCTG	1033
Qy	721	AGAACATAAACTTACATCTCCCTTCCCGAGCAAGGAGCTGGTGAAGCCACAAAAACA	780
Db	1034	AGAACATAAACTTACATCTCCCTTCCCGAGCAAGGAGCTGGCGAAGCCACAAAAACA	1093
Qy	781	TTGCTGCATAGTCTTGGGACTTGGCCAGGAGCTGTTTCAGCATGAGAGCTGGAGTGAC	840
Db	1094	TTGCTGCATAGTCTTGGGACTTGGCCAGGAGCTGTTTCAGCATGAGAGCTGGAGTGAC	1153
Qy	841	ATGCGACAGGAGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCTCCACCAAATC	900
Db	1154	ATGCGACAGGAGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCTCCACCAAATC	1213
Qy	901	TACCAGGCTGTGCTCGTATTGTCTGGGGCATCCGAGGAGGGGGGCTGGAAGTCAAG	960
Db	1214	TACCAGGCTGTGCTCGTATTGTCTGGGGCATCCGAGGAGGGGGGCTGGAAGTCAAG	1273
Qy	961	TCTCTCAACTTGGTATGAGGACAACAACACTCAAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1020
Db	1274	TCTCTCAACTTGGTATGAGGACAACAACACTCAAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1333
Qy	1021	GAGATGCTGAAACCTTCTATGACAACTCTACAATCTCTTACTGCAATGATTTGATGAAG	1080
Db	1334	GAGATGCTGAAACCTTCTATGACAACTCTACAATCTCTTACTGCAATGATTTGATGAAG	1393
Qy	1081	AATTTGAGTCTAGTCTCTCTTTCCGSCATTAFTCTGGAAGCTCTGAAGCCGCTGCTGTT	1140
Db	1394	AATTTGAGTCTAGTCTCTCTTTCCGSCATTAFTCTGGAAGCTCTGAAGCCGCTGCTGTT	1453
Qy	1141	GGGAAGATCCTGTATACACTGACACTCCAGCCACAGGCAAGGTCATGGCTGAGGTGAAC	1200
Db	1454	GGGAAGATCCTGTATACACTGACACTCCAGCCACAGGCAAGGTCATGGCTGAGGTGAAC	1513
Qy	1201	AAGACCTTCAGGAATCGCTGTGTTCATGATCTGGAAGCATGTGGGAGGAACCTCAGC	1260
Db	1514	AAGACCTTCAGGAATCGCTGTGTTCATGATCTGGAAGCATGTGGGAGGAACCTCAGC	1573
Qy	1361	CCCAAGATCTGGACCTTCATGTGAGAACACGCCAAGAAATGTGACCTTGTCCCGATGCTGTG	1320

Db	1574	CCCAAGATCTCGACCTTTCATGGAGAACAGCCAAAGAAATGGACCTTGTCGGATGCTGGTTC	1633
Qy	1321	GACAGCAGGACAAATGACCACTTTTGGGACACAGCTGGATGGCTTAGATTGGACAGCC	1380
Db	1634	GACAGCAGGACAAATGACCACTTTTGGGAAACAGAGTTGGATGGCTTAGATTGGACAGCC	1693
Qy	1381	CAAGACATCGTGGCGTTTTTGGCCAAAGCACCCAGAGAGTGTCCAGTCCAGTAATGGTTCT	1440
Db	1694	CAAGACATCGTGGCGTTTTTGGCCAAAGCACCCAGAGAGTGTCCAGTCCAGTAATGGTTCT	1753
Qy	1441	GTGTACACTGGAGAGAGCTTTCAAGGAGACTTAACAGGCAATCCGAGCAATATCTCGC	1500
Db	1754	GTGTACACTGGAGAGAGCTTTCAAGGAGACTTAACAGGCAATCCGAGCAATATCTCGC	1813
Qy	1501	TTTACTGGAGTGTCTCAACCTGAAACAGCTAGAACCCATAGCAACAGAAAGTTGGCTCATC	1560
Db	1814	TTTACTGGAGTGTCTCAACCTGAAACAGCTAGAACCCATAGCAACAGAAAGTTGGCTCATC	1873
Qy	1561	AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTTCTGGGCTGGTATTGTTCACATGGA	1620
Db	1874	AACAAGTCCATGGAGCTGCTGGATGAGAGAAAGTTCTGGGCTGGTATTGTTCACATGGA	1933
Qy	1621	ATTACTCCAGCAGCATTTGAGCTGCCCATCATGCTCAAGTACAAGATCCGAATGACATTT	1680
Db	1934	ATTACTCCAGCAGCATTTGAGCTGCCCATCATGCTCAAGTACAAGATCCGAATGACATTT	1993
Qy	1681	GACAAATGTGGAGAGGACAAATAAAATCAAGGATGGTACTTGGACCCCTGGTCCCTGAGCT	1740
Db	1994	GACAAATGTGGAGAGGACAAATAAAATCAAGGATGGTACTTGGACCCCTGGTCCCTGAGCT	2053
Qy	1741	GACCCCTTTGAGGACATCGCGTAGCTGTGGGGGGCTTGCCTACTTTCAGAGATGTGGTG	1800
Db	2054	GACCCCTTTGAGGACATCGCGTAGCTGTGGGGGGCTTGCCTACTTTCAGAGATGTGGTG	2113
Qy	1801	GAGCAGGCAATCATCAGGGTGCTCAGGGGCACCGGACGAGAAAGAACTGGTCTATATGCAA	1860
Db	2114	GAGCAGGCAATCATCAGGGTGCTCAGGGGCACCGGACGAGAAAGAACTGGTCTATATGCAA	2173
Qy	1861	CAGATGCCCTATCCCTGTACGTTGATGACATCTTCTCGGGGTGATGAGCGGTGCAATG	1920
Db	2174	CAGATGCCCTATCCCTGTACGTTGATGACATCTTCTCGGGGTGATGAGCGGTGCAATG	2233
Qy	1921	CCCTCTTTCATGACGCTGGGCTGGATTTACTCAGTGGCTGATCATCAAGGGATCGTG	1980
Db	2234	CCCTCTTTCATGACGCTGGGCTGGATTTACTCAGTGGCTGATCATCAAGGGATCGTG	2293
Qy	1981	TATGAGAGGAGGACAGGCTGAAAGAGACCATCGGATCATGGGCTGGACAAAGCATAT	2040
Db	2294	TATGAGAGGAGGACAGGCTGAAAGAGACCATCGGATCATGGGCTGGACAAAGCATAT	2353
Qy	2041	CTCTGGTTTACGTGGTTTCATTAGTAGCCTCATTCCTCTTGTGTGAGGGCTGGGCTGCTA	2100
Db	2354	CTCTGGTTTACGTGGTTTCATTAGTAGCCTCATTCCTCTTGTGTGAGGGCTGGGCTGCTA	2413
Qy	2101	GTGGTATCTCTGAAGTTAGGAACCTGCTGGCCTACAGTGATCCGAGGTTGGTGTGTC	2160
Db	2414	GTGGTATCTCTGAAGTTAGGAACCTGCTGGCCTACAGTGATCCGAGGTTGGTGTGTC	2473
Qy	2161	TTCCGTCCGTTGTTGCTGTGGTGACAACTCTCAGTGGCTTCTGATTAGCACACTCTTC	2220
Db	2474	TTCCGTCCGTTGTTGCTGTGGTGACAACTCTCAGTGGCTTCTGATTAGCACACTCTTC	2533
Qy	2221	TCCAGAGCCAACTGGCAGCAGCCTGTGGGGGATCATCTACTTCACGCTTACTCGTCC	2280
Db	2534	TCCAGAGCCAACTGGCAGCAGCCTGTGGGGGATCATCTACTTCACGCTTACTCGTCC	2593
Qy	2281	TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTGGCTAGC	2340
Db	2594	TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTGGCTAGC	2653
Qy	2341	CTGCTGTCTCTGTGGCTTTTGGTTGGCTTGGTGTGAGTACTTTTGCCTTTTTCAGGAGCAG	2400

Db 2654 CTGCTGTCCTCTGCTGGCTTTTGGGTTTGCTGTGAGTACTTTTGGCCCTTTTGGAGGACG 2713
QY 2401 GCANTTGGAGTCAGTGGGACAACTGTTGAGAGTCCCTGTGGAGGAAGATGGCTTCAAT 2460
Db 2714 GGCATGGAGTCAGTGGGACAACTGTTGAGAGTCCCTGTGGAGGAAGATGGCTTCAAT 2773
QY 2461 CTCACACTTCGATCTCCATGATGCTGTTTGACACCTTCCCTATGAGGAGTATGACCTGG 2520
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Db 2954 AAGAGAATATCAGAAATCTGATGAGGAGGAACCCACCCACTTGAAGCTGGCGTGTCC 3013
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QY 2761 CTGAATTTTATGAGGCCAGATCACTCCCTTCTTGGGCCCAATGGAGCGGGGAAGACG 2820
Db 3074 CTGAATTTTATGAGGCCAGATCACTCCCTTCTTGGGCCCAATGGAGCGGGGAAGACG 3133
QY 2821 ACCACATGTCATCTGACCGGGTGTTCCTCCCGGACTCGGGCACCGCTACATCCCTG 2880
Db 3134 ACCACATGTCATCTGACCGGGTGTTCCTCCCGGACTCGGGCACCGCTACATCCCTG 3193
QY 2881 GGAAGAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTTGGGGGTCTGCCCCAG 2940
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QY 2941 CATACGTCGCTGTTGACATGCTGACTCTGAAGAACACATCTGTTCTATGCCGCTTG 3000
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QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACACAGCCAGCTGTGAGTGGAAATCAGAGAAAG 3120
Db 3374 TTGCCATCAAGCAAGCTGAAAGCAAAACACAGCCAGCTGTGAGTGGAAATCAGAGAAAG 3433
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QY 3181 GCTGTGTGGACCCCTTACTCCCGAGGGGAATATGGGAGCTGTGCTGGAATATCCGACAA 3240
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QY 3241 GSCCGCACCATTTCTCTACACACACATGGATGAAGCGGAGCTCCTGGGGACAGG 3300
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RESULT 10

US-09-984-827-115

; Sequence 115, Application US/09984827

; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFELE, PATRICE

; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

; FILE REFERENCE: 03806.0522-00000

; CURRENT APPLICATION NUMBER: US/09/984,827

; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/254,108

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: FR 00/14037

; PRIOR FILING DATE: 2000-10-31

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 115

; LENGTH: 9870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (7138)

; OTHER INFORMATION: a, t, c or g

US-09-984-827-115

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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RESULT 11

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US-09-984-827-119
; Sequence 119, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFFLE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; TITLE OF INVENTION: DETECTION-METHODS AND KITS THEREFOR
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FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 119
LENGTH: 9870
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (7138)
OTHER INFORMATION: a, t, c or g
US-09-984-827-119

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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RESULT 12

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; Publication No. US20030056234A1

; GENERAL INFORMATION:

; APPLICANT: DENEFFLE, PATRICE

; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

; APPLICANT: ARNOULD-REGUIGNE, ISABELLE

; APPLICANT: DUVERGER, NICOLAS

; APPLICANT: CAMBIEN, FRANCOIS

; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND

; FILE REFERENCE: 03806.0522-00000

; CURRENT APPLICATION NUMBER: US/09/984, 827

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; SOFTWARE: PatentIn Ver. 2.1

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; LENGTH: 9870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: modified_base

; LOCATION: (7138)

; OTHER INFORMATION: a, t, c or g

US-09-984-827-120

Query Match	99.7%	Score 6764.8	DB 9	Length 9870
Best Local Similarity	99.8%	Pred. No. 0		
Matches 6772	Conservative	0	Indels 12	Gaps 0
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QY	241	TGTTTCGGTTACCCGACTCCTCGGGAGGCTCCCGAGTGTGGAACTTTAAACAAATCC	300	
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QY	301	ATTGTGGCTCGCTGTTCTCAGATGCTCGGAGGCTCTTTTATACAGCCAGAAAGACACC	360	
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QY	481	AACTCTCTCTCCAAAGTCTACTGTGGACAGATGCTGAGGCTGATGTCATCTCCAC	540	
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QY	541	AAGGTATTTTGAAGGCTACCAAGTTCATTTGACAAAGTCTGTGCAATGGATCAAAATCA	600	
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Db	1934	ATTACTCCAGGACGATGAGCTGCCCATCATGTCAAGTACAAGATCCGAATGACATTT	1993
QY	1681	GACAATGTGGAGAGGACAAATAAATCAAGATGGTACTGGGACCCCTGGCTCGAGCT	1740
Db	1994	GACAATGTGGAGAGGACAAATAAATCAAGATGGTACTGGGACCCCTGGCTCGAGCT	2053
QY	1741	GACCCCTTTGAGGACATGGGTACGTCTGGGGGGCTTTCGCTACTTGCAGGATGGTG	1800
Db	2054	GACCCCTTTGAGGACATGGGTACGTCTGGGGGGCTTTCGCTACTTGCAGGATGGTG	2113
QY	1801	GAGCAGCAATCATCAGGCTGCTGACGGCCACCGAGAGAAACTGGTGTCTATATGCAA	1860
Db	2114	GAGCAGCAATCATCAGGCTGCTGACGGCCACCGAGAGAAACTGGTGTCTATATGCAA	2173
QY	1861	CAGATGCCCTATCCCTGTTTACCTTGTGATGACATCTTTCTCGGGGTGATGAGCCGTCATG	1920
Db	2174	CAGATGCCCTATCCCTGTTTACCTTGTGATGACATCTTTCTCGGGGTGATGAGCCGTCATG	2233
QY	1921	CCCTCTTCATGACCGTGGCTTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1980
Db	2234	CCCTCTTCATGACCGTGGCTTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	2293
QY	1981	TATGAGAAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGGCTTGACAAACAGCAT	2040
Db	2294	TATGAGAAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGGCTTGACAAACAGCAT	2353
QY	2041	CTCTGGTTTACGTGGTTCATTAAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCTGCTA	2100
Db	2354	CTCTGGTTTACGTGGTTCATTAAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCTGCTA	2413
QY	2101	GTGGTCACTCCTCAAGTTAGGAACCTGCTGCCCTACAGTATCCAGCGGTGGTGTTC	2160

Db 2414 GTGGTCATCTCCTGAAGTATAGAAACCTGCTGCGCCCTACAGTGATCCAGCGTGGTGTTC 2473
QY 2161 TTCCTGTCGGTGTTCCTGCTGGTGACAACTCCCTGACAGTGTCTCCTGATTAGCACACTTC 2220
Db 2474 TTCCTGTCGGTGTTCCTGCTGGTGACAACTCCCTGACAGTGTCTCCTGATTAGCACACTTC 2533
QY 2221 TCCAGAGCCAACTGGCAGCACACCTGTGGGGGCATCATCTACTTACCGTGTACCTGGCC 2280
Db 2534 TCCAGAGCCAACTGGCAGCACACCTGTGGGGGCATCATCTACTTACCGTGTACCTGGCC 2593
QY 2281 TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCCTGCTAGC 2340
Db 2594 TACGTCCTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCCTGCTAGC 2653
QY 2341 CTGCTGTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTTGGCCCTTTTGGAGAGCAG 2400
Db 2654 CTGCTGTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTTGGCCCTTTTGGAGAGCAG 2713
QY 2401 GGCATTGGAGTGCAGTGGGACAACTGTTTGGAGCTCTCTGAGAGGAAGATGGCTTCAAT 2460
Db 2714 GGCATTGGAGTGCAGTGGGACAACTGTTTGGAGCTCTCTGAGAGTCTCTGAGAGGAAGATGGCTTCAAT 2773
QY 2461 CTCACACTTCGATCTCCATGATGCTGTTTGGACACCTTCTCTATGGGGTGTATGACCTGG 2520
Db 2774 CTCACACTTCGATCTCCATGATGCTGTTTGGACACCTTCTCTATGGGGTGTATGACCTGG 2833
QY 2521 TACATTGAGCTGTCTTCCAGGCCAGTACGGAATTCAGGCCCTGCTATTTCCTTTC 2580
Db 2834 TACATTGAGCTGTCTTCCAGGCCAGTACGGAATTCAGGCCCTGCTATTTCCTTTC 2893
QY 2581 ACCAAGTCTACTGGTGTGGCGAGGAAGTGTATGAGAAGAGCACCTCGTGTTCACACAG 2640
Db 2894 ACCAAGTCTACTGGTGTGGCGAGGAAGTGTATGAGAAGAGCACCTCGTGTTCACACAG 2953
QY 2641 AAGAGATGTGAGAATCTGATGAGAGGAGAACCCACCTGGAAGCTGGGCGTGTCC 2700
Db 2954 AAGAGATATCAGAATCTGATGAGAGGAGAACCCACCTGGAAGCTGGGCGTGTCC 3013
QY 2701 ATTCAAGACCTGGTAAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCCTGGCA 2760
Db 3014 ATTCAAGACCTGGTAAAAGTCTACCGAGATGGATGAAGTGGCTGTGATGGCCCTGGCA 3073
QY 2761 CTGAATTTTATGAGGCGCAGATACCTCTCTTCCCTGGGCGCACAATGGAGCGGGGAGACG 2820
Db 3074 CTGAATTTTATGAGGCGCAGATACCTCTCTTCCCTGGGCGCACAATGGAGCGGGGAGACG 3133
QY 2821 ACCACATGTCAATCTGACCGGGTGTTCCTCCCGACCTCGGGCACCGCTACATCTCG 2880
Db 3134 ACCACATGTCAATCTGACCGGGTGTTCCTCCCGACCTCGGGCACCGCTACATCTCG 3193
QY 2881 GGAAAGACATTCGCTCTGATGATGACCACTCCGGCGAGAACCTTGGGGGTCTGTCCCGAG 2940
Db 3194 GGAAAGACATTCGCTCTGATGATGACCACTCCGGCGAGAACCTTGGGGGTCTGTCCCGAG 3253
QY 2941 CATACGTGCTGTGATGATGCTGACTGCGAAGAACACATCTGGTTCATGCGCGCTTG 3000
Db 3254 CATACGTGCTGTGATGATGCTGACTGCGAAGAACACATCTGGTTCATGCGCGCTTG 3313
QY 3001 AAAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3060
Db 3314 AAAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3373
QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGAGGTGGAATGACAGAGAAG 3120
Db 3374 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTGAGGTGGAATGACAGAGAAG 3433
QY 3121 CTATCTGTGGCCCTTGGCCCTTTGCGGGGATCTAAGGTTGTCAATCTGGATGAACCCACA 3180
Db 3434 CTATCTGTGGCCCTTGGCCCTTTGCGGGGATCTAAGGTTGTCAATCTGGATGAACCCACA 3493
QY 3181 GCTGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGTGCTGTAATACCGACA 3240
Db 3494 GCTGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGTGCTGTAATACCGACA 3553

QY 3241 GGCGCACCATTTATTTCTCTACACACCATGGATGAAGCGGACGTCCTGGGGACAGG 3300
Db 3354 GGCGCACCATTTATTTCTCTACACACCATGGATGAAGCGGACGTCCTGGGGACAGG 3613
QY 3301 ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGGCTCCTCCCTGTTCTTGAAGAAC 3360
Db 3614 ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGGCTCCTCCCTGTTCTTGAAGAAC 3673
QY 3361 CAGCTGGGAACAGGCTACTACTGACCTTGGTCAAGAAAGATGTGAATCCTCCCTCAGT 3420
Db 3674 CAGCTGGGAACAGGCTACTACTGACCTTGGTCAAGAAAGATGTGAATCCTCCCTCAGT 3733
QY 3421 TCCTGCAGAAACAGTAGTAGCTGTGTCTATCTGAAAAAGGAGGACAGTGTTCCTCAG 3480
Db 3734 TCCTGCAGAAACAGTAGTAGCTGTGTCTATCTGAAAAAGGAGGACAGTGTTCCTCAG 3793
QY 3481 AGCAGTTCTGATGTGCTGGCGAGCGACCATGAGAGTGCACAGCTGACCATCGATGTC 3540
Db 3794 AGCAGTTCTGATGTGCTGGCGAGCGACCATGAGAGTGCACAGCTGACCATCGATGTC 3853
QY 3541 TCTGCTATCTCCAACTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGTGTGAAGACATA 3600
Db 3854 TCTGCTATCTCCAACTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGTGTGAAGACATA 3913
QY 3601 GGGCATGAGCTGACCTATGTCTGCCATATGAAGCTGCTAAGGAGGAGGCTTTGTGGAA 3660
Db 3914 GGGCATGAGCTGACCTATGTCTGCCATATGAAGCTGCTAAGGAGGAGGCTTTGTGGAA 3973
QY 3661 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGSCATCTCA 3720
Db 3974 CTCTTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTTCTAGTTATGSCATCTCA 4033
QY 3721 GAGAGACCTTGGNAGAAATATTCTCAAGGTGGCCGAAAGAGAGTGGGTGGATGCTGAG 3780
Db 4034 GAGAGACCTTGGNAGAAATATTCTCAAGGTGGCCGAAAGAGAGTGGGTGGATGCTGAG 4093
QY 3781 ACCTCAGATGCTACCTTCCAGCAAGACGAAACAGCGGGCTTCGGGCAACAGCAGAGC 3840
Db 4094 ACCTCAGATGCTACCTTCCAGCAAGACGAAACAGCGGGCTTCGGGCAACAGCAGAGC 4153
QY 3841 TGTCTTCCCGCTTCACTGAAGATGATGCTGTGATCCAAATGATTCGACATGACCCCA 3900
Db 4154 TGTCTTCCCGCTTCACTGAAGATGATGCTGTGATCCAAATGATTCGACATGACCCCA 4213
QY 3901 GAATCCAGAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAAAGGGTCTTACCAGGTGAAA 3960
Db 4214 GAATCCAGAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAAAGGGTCTTACCAGGTGAAA 4273
QY 3961 GGCTGGAAACTTACACAGCAACAGTGTGGTGGCCCTTTTGTGGAAGAGACTGCTAAATGTC 4020
Db 4274 GGCTGGAAACTTACACAGCAACAGTGTGGTGGCCCTTTTGTGGAAGAGACTGCTAAATGTC 4333
QY 4021 AGCGGAGTCCGAAAGGATTTTGTGCTCAGATGCTGTGCGACGCTGTGTTGCTGCATT 4080
Db 4334 AGCGGAGTCCGAAAGGATTTTGTGCTCAGATGCTGTGCGACGCTGTGTTGCTGCATT 4393
QY 4081 GCGCTTGTCTGACGCTGTGCTGCCACCTTTTGGCAAGTACCCAGCCCTGGAACTTCAG 4140
Db 4394 GCGCTTGTCTGACGCTGTGCTGCCACCTTTTGGCAAGTACCCAGCCCTGGAACTTCAG 4453
QY 4141 CCCTGGATGTACACGACAGTACACATTTGTCAGCAATGATGCTCTGAGGACAGGGA 4200
Db 4454 CCCTGGATGTACACGACAGTACACATTTGTCAGCAATGATGCTCTGAGGACAGGGA 4513
QY 4201 ACCCTGGAACCTTAAACGCCCTTACCAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA 4260
Db 4514 ACCCTGGAACCTTAAACGCCCTTACCAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA 4573
QY 4261 GGAACCCATCCAGACACGCGCTGCCAGGAGGGGAGGAAGTGGACCATGCCCCA 4320
Db 4574 GGAACCCATCCAGACACGCGCTGCCAGGAGGGGAGGAAGTGGACCATGCCCCA 4633

Qy	4321	GTTC	CCCCAGAC	CAATC	ATGGAC	CTCTTC	CCAGAA	TGGGA	CTGGACA	ATGCA	AGACCCCTTCA	4380
Db	4634	GTTC	CCCCAGAC	CAATC	ATGGAC	CTCTTC	CCAGAA	TGGGA	CTGGACA	ATGCA	AGACCCCTTCA	4693
		CTTG	CAATG	CGATG	AGAGAT	CTCA	AGAAAT	CTGCTG	CTGCTG	CTGCTG	CTGCTG	CTGCTG
Qy	4381	CTTG	CAATG	CGATG	AGAGAT	CTCA	AGAAAT	CTGCTG	CTGCTG	CTGCTG	CTGCTG	4440
Db	4694	CTTG	CAATG	CGATG	AGAGAT	CTCA	AGAAAT	CTGCTG	CTGCTG	CTGCTG	CTGCTG	4753
Qy	4441	GCAG	GGGGG	GGCTC	CTCC	TCCAC	AAAGAA	AAAAA	CAACAC	TA	CTCTTC	4500
Db	4754	GCAG	GGGGG	GGCTC	CTCC	TCCAC	AAAGAA	AAAAA	CAACAC	TA	CTCTTC	4813
Qy	4501	ACAG	GAAGAA	AAACAT	TTCC	GAATTA	TCGTG	GAAGAC	GTATG	TCGACAG	TATAG	4560
Db	4814	ACAG	GAAGAA	AAACAT	TTCC	GAATTA	TCGTG	GAAGAC	GTATG	TCGACAG	TATAG	4873
Qy	4561	TTAA	GAACA	CAAGAT	CTGG	TGAAT	GAGTTT	AGTAT	GATGG	CGCTTT	CCCTCG	4620
Db	4874	TTAA	GAACA	CAAGAT	CTGG	TGAAT	GAGTTT	AGTAT	GATGG	CGCTTT	CCCTCG	4933
Qy	4621	AA	TACTCA	AGC	ACTTCC	TCCG	AGTCA	AGAG	TTA	TGATG	CCATCA	4680
Db	4934	AA	TACTCA	AGC	ACTTCC	TCCG	AGTCA	AGAG	TTA	TGATG	CCATCA	4993
Qy	4681	CAC	CTAA	AGCTG	CCCA	AGAC	AGTTTCT	CGATC	ATG	TC	CAAC	4740
Db	4994	CAC	CTAA	AGCTG	CCCA	AGAC	AGTTTCT	CGATC	ATG	TC	CAAC	5053
Qy	4741	ATG	AC	AGG	AGCTG	GCAC	AC	AGAA	TAAT	GTCA	AGGTG	4800
Db	5054	ATG	AC	AGG	AGCTG	GCAC	AC	AGAA	TAAT	GTCA	AGGTG	5113
Qy	4801	GCA	ATC	AG	CTTCT	CC	TGAA	TGTC	ATCA	CAATG	CCATTC	4860
Db	5114	GCA	ATC	AG	CTTCT	CC	TGAA	TGTC	ATCA	CAATG	CCATTC	5173
Qy	4861	GG	AGAA	CCCT	TAG	CC	CAATTA	TGGA	ATTA	TGCTTT	CAATCA	4920
Db	5174	GG	AGAA	CCCT	TAG	CC	CAATTA	TGGA	ATTA	TGCTTT	CAATCA	5233
Qy	4921	CAG	CA	CTC	AC	AGGTG	GCCTCG	TATG	ATC	ACCA	CA	4980
Db	5234	CAG	CA	CTC	AC	AGGTG	GCCTCG	TATG	ATC	ACCA	CA	5293
Qy	4981	GT	CAT	TTT	TG	CAATG	TG	CGAAT	TG	CGCTT	CAATCA	5040
Db	5294	GT	CAT	TTT	TG	CAATG	TG	CGAAT	TG	CGCTT	CAATCA	5353
Qy	5041	GT	CAG	AA	CA	AAAC	CA	CCCTG	CA	GTG	AGT	5100
Db	5354	GT	CAG	AA	CA	AAAC	CA	CCCTG	CA	GTG	AGT	5413
Qy	5101	TCT	AAT	TTT	TG	CTG	GGAT	TG	TC	CAAT	TG	5160
Db	5414	TCT	AAT	TTT	TG	CTG	GGAT	TG	TC	CAAT	TG	5473
Qy	5161	TT	CAT	CTG	CTT	CCAG	CAG	AGT	CCCTAT	GTG	CTC	5220
Db	5474	TT	CAT	CTG	CTT	CCAG	CAG	AGT	CCCTAT	GTG	CTC	5533
Qy	5221	CT	ACT	TTT	TG	CTG	TG	GGT	GGTCA	ATCA	CAC	5280
Db	5534	CT	ACT	TTT	TG	CTG	TG	GGT	GGTCA	ATCA	CAC	5593
Qy	5281	AGA	T	CCCC	AG	CAC	AGC	CTAT	GTG	TG	CTC	5340
Db	5594	AGA	T	CCCC	AG	CAC	AGC	CTAT	GTG	TG	CTC	5653
Qy	5341	GG	CAG	CTG	GC	CA	CC	CTT	GTG	TG	CTC	5400
Db	5654	GG	CAG	CTG	GC	CA	CC	CTT	GTG	TG	CTC	5713
Qy	5401	GAT	AT	CTG	AA	GT	CCG	TG	TTCT	TG	AT	5460

Db	5714		GATATCTGAAGTCCGCTGTTCTTGATCTTCCACATTTTTCCTCGGACGAGGCTCATC	5773
Qy	5461		GACATGTTGAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGAGAAATCGCTTT	5520
Db	5774		GACATGTTGAAAACACGAGCAATGGCTGATGCCCTGGAAAGTTTGGGAGAAATCGCTTT	5833
Qy	5521		GTGTCACCAATATCTTTGGGACTTTGTGGGACGAAACCTCTTTCGGCATGGCCGTGGAAAGG	5580
Db	5834		GTGTCACCAATATCTTTGGGACTTTGTGGGACGAAACCTCTTTCGGCATGGCCGTGGAAAGG	5893
Qy	5581		GTGCTGTTCTCCTCATTACTGTTCTGATCCAGTACAGATCTTTCATCAGGCCACAGACCT	5640
Db	5894		GTGCTGTTCTCCTCATTACTGTTCTGATCCAGTACAGATCTTTCATCAGGCCACAGACCT	5953
Qy	5641		GTAATCCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	5700
Db	5954		GTAATCCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAG	6013
Qy	5701		AGAAATCTTCATGCTGGAGGCCAGATGACATCTTTAGAAATCAAGGAGTTGACGAAGATA	5760
Db	6014		AGAAATCTTCATGCTGGAGGCCAGATGACATCTTTAGAAATCAAGGAGTTGACGAAGATA	6073
Qy	5761		TATAGAAGGAAGCGGAAGCCTGCTGTTTGACAGGATTTGCGTGGGCATTCCTCTGGTGGAG	5820
Db	6074		TATAGAAGGAAGCGGAAGCCTGCTGTTTGACAGGATTTGCGTGGGCATTCCTCTGGTGGAG	6133
Qy	5821		TGCTTTGGGCTCTGGAGTTTAATGGGCTGAAAATCATCAACTTTCAGATGTTTAAACA	5880
Db	6134		TGCTTTGGGCTCTGGAGTTTAATGGGCTGAAAATCATCAACTTTCAGATGTTTAAACA	6193
Qy	5881		GGAGATACCACTGTTTACCAGAGAGATGCTTTCCTTTACAAAAATAGTATCTTATCAAAAC	5940
Db	6194		GGAGATACCACTGTTTACCAGAGAGATGCTTTCCTTTACAAAAATAGTATCTTATCAAAAC	6253
Qy	5941		ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCAGAGACTG	6000
Db	6254		ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCAGAGACTG	6313
Qy	6001		TTGACTGGGAGAGAACACGTGGAGTTCTTTTGCCCTTTTGAGAGAGTCCCAGAGAAAGAA	6060
Db	6314		TTGACTGGGAGAGAACACGTGGAGTTCTTTTGCCCTTTTGAGAGAGTCCCAGAGAAAGAA	6373
Qy	6061		GTTCGCAAGGTTTGAGTGGGCGGATTCGGAACATGGGCCCTCGTGAAGTATGGAGAAAAA	6120
Db	6374		GTTGGCAAGGTTTGAGTGGGCGATTCGGAACATGGGCCCTCGTGAAGTATGGAGAAAAA	6433
Qy	6121		TATCCTGGTAACTATAGTGGAGCAACAACGCCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6434		TATCCTGGTAACTATAGTGGAGCAACAACGCCAAGCTCTCTACAGCCATGGCTTTGATC	6493
Qy	6181		GGCGGGCCTCCTGCTGTTCTTCTGATGAACCCACACAGGCATGGATCCCAAAGCCCGG	6240
Db	6494		GGCGGGCCTCCTGCTGTTCTTCTGATGAACCCACACAGGCATGGATCCCAAAGCCCGG	6553
Qy	6241		CGGTTCTGTGGAAATGTGCCCTTAAGCTTTGTCAGGAGGGAGATCAGTAGTCTTACA	6300
Db	6554		CGGTTCTGTGGAAATGTGCCCTTAAGCTTTGTCAGGAGGGAGATCAGTAGTCTTACA	6613
Qy	6301		TCTCATAGTATGGAAGAATGTGAAGCTTCTTGCACTAGGATGGCAATCATGGTCAATGGA	6360
Db	6614		TCTCATAGTATGGAAGAATGTGAAGCTTCTTGCACTAGGATGGCAATCATGGTCAATGGA	6673
Qy	6361		AGGTTTCAGGTCCTTGGCAGTGTCACAGATCTTAAAAATAGGTTTGGAGATGGTTATACA	6420
Db	6674		AGGTTTCAGGTCCTTGGCAGTGTCACAGATCTTAAAAATAGGTTTGGAGATGGTTATACA	6733
Qy	6421		ATAGTTGTACCAATAGCAGGGTCCAAACCCGGACCTGAAGCCCTGTCAGGATTTCTTTGGA	6480
Db	6734		ATAGTTGTACCAATAGCAGGGTCCAAACCCGGACCTGAAGCCCTGTCAGGATTTCTTTGGA	6793
Qy	6481		CTTGCAATTCCTGGAAAGTGTCTTAAAGAGAAACACCGGAAACATGCTCAATATCACAGCTT	6540

QY 1321 GACAGCAGGACAAATGACCACTTTTGGGAACAGCAGATGGTGTAGATTGACAGCC 1380
Db 1634 GACAGCAGGACAAATGACCACTTTTGGGAACAGCAGATGGTGTAGATTGACAGCC 1693
QY 1381 CAAGACATCGTGGCCGCTTTTGGCCAAAGCACCAGAGGATGCCAGTCAAGTAAGTGTCT 1440
Db 1694 CAAGACATCGTGGCCGCTTTTGGCCAAAGCACCAGAGGATGCCAGTCAAGTAAGTGTCT 1753
QY 1441 GTGTACACCTGGAGAGAGCTTTTCAACGAGACTTAACAGGCAATCCGACCATATCTCGC 1500
Db 1754 GTGTACACCTGGAGAGAGCTTTTCAACGAGACTTAACAGGCAATCCGACCATATCTCGC 1813
QY 1501 TTCTAGGAGTGTCTCAACTGACCAAGCTAGAACCCATAGAACAGAGTCTGGCTCATC 1560
Db 1814 TTCTAGGAGTGTCTCAACTGACCAAGCTAGAACCCATAGAACAGAGTCTGGCTCATC 1873
QY 1561 AACAAGTCCATGAGCTGCTGGATGAGAGGAAATTCGGCTGTGTATGTCTACTGGA 1620
Db 1874 AACAAGTCCATGAGCTGCTGGATGAGAGGAAATTCGGCTGTGTATGTCTACTGGA 1933
QY 1621 ATTACTCCAGGACGATGAGCTGCCCATCATGTCAAGTCAAGATCAAGATCCGAATGACATT 1680
Db 1934 ATTACTCCAGGACGATGAGCTGCCCATCATGTCAAGTCAAGATCAAGATCCGAATGACATT 1993
QY 1681 GACAATGTGAGAGGACAAATAAATCAAGGATGGTACTGGGACCCCTGGTCTCGAGCT 1740
Db 1994 GACAATGTGAGAGGACAAATAAATCAAGGATGGTACTGGGACCCCTGGTCTCGAGCT 2053
QY 1741 GACCCCTTTGAGGACATCGGCTACGCTGTGGGGGGCTTGCCTACTTGCAGGATGTGGT 1800
Db 2054 GACCCCTTTGAGGACATCGGCTACGCTGTGGGGGGCTTGCCTACTTGCAGGATGTGGT 2113
QY 1801 GAGCAGGCAATCATCAGGTGCTGAGGGCACCAGAGAAACCTGGTCTATATGCAA 1860
Db 2114 GAGCAGGCAATCATCAGGTGCTGAGGGCACCAGAGAAACCTGGTCTATATGCAA 2173
QY 1861 CAGATCCCTATCCCTGTTTACGTTGATGACATCTTCTCGGGGTGATGAGCCGGTCAATG 1920
Db 2174 CAGATCCCTATCCCTGTTTACGTTGATGACATCTTCTCGGGGTGATGAGCCGGTCAATG 2233
QY 1921 CCCCTTTGATGAGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 1980
Db 2234 CCCCTTTGATGAGCTGGCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATCGT 2293
QY 1981 TATGAGAGGAGCAGGCTGAAAGAGACCATCGGATCATGGGCTGGACACAGCAT 2040
Db 2294 TATGAGAGGAGCAGGCTGAAAGAGACCATCGGATCATGGGCTGGACACAGCAT 2353
QY 2041 CTCTGTTTGTAGTGTTCATTTAGTAGCCTCATTCCTTCCTTTGTGAGCGCTGGCTGTCTA 2100
Db 2354 CTCTGTTTGTAGTGTTCATTTAGTAGCCTCATTCCTTCCTTTGTGAGCGCTGGCTGTCTA 2413
QY 2101 GTGGTCATCTGAAGTTAGAAACCTGCTGCCCTACAGTATCCAGCGTGTGTTGTC 2160
Db 2414 GTGGTCATCTGAAGTTAGAAACCTGCTGCCCTACAGTATCCAGCGTGTGTTGTC 2473
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Db 2474 TTCTCTCGGTGTTTCTGTGTGACAAATCCTGAGTGTCTTCTGATGACACATCTTC 2533
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QY 2281 TAGCTCTGTGTGTCATGCGAGGACTACGTGGGCTTCCACTCAAGATCTTCGTAGC 2340
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Db 2714 GGCATTGGAGTGCAGTGGGACAACTGTTTGGAGAGTCTCTGGAGGAGATGGCTCAAT 2773
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Db 2774 CTCACCACTTCGATCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGTGACCTGG 2833
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Db 2834 TACATGAGGCTGTCTTTTCCAGGCCAGTAGGAAATTCOCAGGCCCTGTATTTTCTTGC 2893
QY 2581 ACCAAGTCTTACTGTTTGGCGAGGAAAGTATGAGAGAGCCACCTGTTCCCAACAG 2640
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QY 2761 CTGAATTTTATGAGGGCCAGATCACCTCTCTTCTGGGCCACAAATGGAGCGGGGAAGC 2820
Db 3074 CTGAATTTTATGAGGGCCAGATCACCTCTCTTCTGGGCCACAAATGGAGCGGGGAAGC 3133
QY 2821 ACCACCATGTCATCTCTGACCGGGTGTTCGCCCGACCTCGGGCACCCTATCTCTG 2880
Db 3134 ACCACCATGTCATCTCTGACCGGGTGTTCGCCCGACCTCGGGCACCCTATCTCTG 3193
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QY 2941 CATACGTCGTGTTGACATGCTGACTGTGAGAGAACACATCTGGTCTATGCGCGCTTG 3000
Db 3254 CATACGTCGTGTTGACATGCTGACTGTGAGAGAACACATCTGGTCTATGCGCGCTTG 3313
QY 3001 AAAGGGCTCTGAGAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3060
Db 3314 AAAGGGCTCTGAGAGCACGTGAAGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT 3373
QY 3061 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGAAATGCAGAGAAAG 3120
Db 3374 TTGCCATCAAGCAAGCTGAAAGCAAAACAGCCAGCTGTCAAGTGGAAATGCAGAGAAAG 3433
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Db 3434 CTATCTGGCCCTTGGCCCTTGTGCGGGGATCTAGGTTGTCTCTGATGAGACCCACA 3493
QY 3181 GCTGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3240
Db 3494 GCTGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA 3553
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Db 3554 GSCCGCACCATTTATCTCTACACACCATGATGATGAAGCGGAGCTCTGGGGACAGG 3613
QY 3301 ATTGCATCATCTCCCATGGGAAGCTGTGTGGGCTCTCTGCTGTTCTGAAGAAC 3360
Db 3614 ATTGCATCATCTCCCATGGGAAGCTGTGTGGGCTCTCTGCTGTTCTGAAGAAC 3673
QY 3361 CAGCTGGGAACAGGTACTACTGACCTGTGGTCAAGAAAGATGTGGAATTCCTCCCTCAGT 3420
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Db 3794 AGCAGTTCTGATGCTGGCCCTGGCAGCGACCATTGAGAGTGACACGGTGACCATCGATGTC 3853
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Db 3854 TCTGCTATCTCCAACTCATCAGGAGCATGTGCTGAAGCCCGCTGTGGAACACATA 3913
Qy 3601 GGCATGAGCTGACCTATGCTGCCATATGAAGCTGCTGAAGGAGGAGCCCTTTGTGAA 3660
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Qy 3661 CTTCTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTAGTTATGGCATCTCA 3720
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Qy 3781 ACCTCAGATGGTACCTTGCACGAGACGAAACAGCGCGGCTTCGGGACAGCAGAGC 3840
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Qy 4141 CCTGGATGTACAAGAAACAGTACATTTGTGCAATATGATGCTCTGAGGACACGGGA 4200
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Qy 4261 GGAACCCCAATCCAGACACGCGCTTCCAGGCGAGGAGAGAGTGGACACTGCCCA 4320
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Qy 4381 CTTGATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCTGTGTGCCCCAGGG 4440
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Qy 4501 ACAGGAACAAACATTTCCGATATCTGTGGAAGAGCTGATGCGAGATCATAGCCAAAGC 4560
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Db 4874 TTAAGAACAAAGATCTGGGTGAATGAGTTTATGATGCGGCTTTTCCCTGGGTGTCAGT 4933

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; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
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; CURRENT APPLICATION NUMBER: US/09/984.827
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; LENGTH: 9870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (7138)
; OTHER INFORMATION: a, t, c or g
US-09-984-827-122
Query Match 99.7%; Score 5764.8; DB 9; Length 9870;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db 4094 ACCTCAGATGGTACCTTGCCAGCAAGCAAGCAAGCGGCGCTTCGGGACAGCAGACG 4153
QY 3841 TGTCTTCGCCCGTTCACCTGAGATGATGCTGCTGATCCAAATGATCTGACATAGACCCA 3900
Db 4154 TGTCTTCGCCCGTTCACCTGAGATGATGCTGCTGATCCAAATGATCTGACATAGACCCA 4213
QY 3901 GAATCCAGAGACAGACACTTGTCTCAGTGGGATGGATGGCAAGGGTCTTACCAGSTGAAA 3960
Db 4214 GAATCCAGAGACAGACACTTGTCTCAGTGGGATGGATGGCAAGGGTCTTACCAGSTGAAA 4273
QY 3961 GGCTGGAACCTTACACAGAACAGTTTGTGGCCCTTTTGTGGAGAGACTGCTAAATGCC 4020
Db 4274 GGCTGGAACCTTACACAGAACAGTTTGTGGCCCTTTTGTGGAGAGACTGCTAAATGCC 4333
QY 4021 AGACGGAGTCGGAAGAGATTTTGTCTCAGATGTCTTGCCAGCTGTGTTGTCTGCATT 4080
Db 4334 AGACGGAGTCGGAAGAGATTTTGTCTCAGATGTCTTGCCAGCTGTGTTGTCTGCATT 4393
QY 4081 GCCCTTGTGTTCAGCCCTGATGCTGCCACCTTTTGGCAAGTACCCAGCCTGGAACTTCAG 4140
Db 4394 GCCCTTGTGTTCAGCCCTGATGCTGCCACCTTTTGGCAAGTACCCAGCCTGGAACTTCAG 4453
QY 4141 CCTTGGATGTACACAGAACAGTACACATTTGTGAGCAATGATGCTCTGAGGACACGGGA 4200
Db 4454 CCTTGGATGTACACAGAACAGTACACATTTGTGAGCAATGATGCTCTGAGGACACGGGA 4513
QY 4201 ACCCTGGAACCTTTAAAGCGCCCTACCAAGACCTTGGCTTCGGGACCCCTGTATGGAA 4260
Db 4514 ACCCTGGAACCTTTAAAGCGCCCTACCAAGACCTTGGCTTCGGGACCCCTGTATGGAA 4573
QY 4261 GGAACCCATCCACAGACACGCTGCCAGCGGAGGAGGAGTGGACCTTGCCCCCA 4320
Db 4574 GGAACCCATCCACAGACACGCTGCCAGCGGAGGAGGAGTGGACCTTGCCCCCA 4633
QY 4321 GTTCCCGACAGCCATCATGAGACCTTCTCCAGAAATGGGAACCTGGACAATGCAGAACCTTCA 4380
Db 4634 GTTCCCGACAGCCATCATGAGACCTTCTCCAGAAATGGGAACCTGGACAATGCAGAACCTTCA 4693
QY 4381 CCTGCATGCCAGTGTAGCAGGACAAAATCAAGAAAGTGTGCTGCTGTGCTCCCGCAGGG 4440
Db 4694 CCTGCATGCCAGTGTAGCAGGACAAAATCAAGAAAGTGTGCTGCTGTGCTCCCGCAGGG 4753
QY 4441 GCAGGGGGCTGCTCCTCCTCCCAAGAAACAAACAACTGCAGATATCCTTTCAGGACCTG 4500
Db 4754 GCAGGGGGCTGCTCCTCCTCCCAAGAAACAAACAACTGCAGATATCCTTTCAGGACCTG 4813
QY 4501 ACAGAGAAACATTTCCGATTTATCTGTTGAAGACGTATGTGCAGATCATAGCCAAAGC 4560
Db 4814 ACAGAGAAACATTTCCGATTTATCTGTTGAAGACGTATGTGCAGATCATAGCCAAAGC 4873
QY 4561 TTAAGAAACAAAGATCTGGGTGAATGAGTTTATGTTAGGTATGGCGCTTTTCCCTGGGTGCTAGT 4620
Db 4874 TTAAGAAACAAAGATCTGGGTGAATGAGTTTATGTTAGGTATGGCGCTTTTCCCTGGGTGCTAGT 4933
QY 4621 AATACTCAAGCACTTCCCTCCAGTCAAGAGTTTATGATGCCATCAACAAATGAAGAAA 4680
Db 4934 AATACTCAAGCACTTCCCTCCAGTCAAGAGTTTATGATGCCATCAACAAATGAAGAAA 4993
QY 4681 CACCTAAAGCTGGCCCAAGGACAGTCTGCAGATGATTTCTCAACAGCTTGGGAAGATT 4740
Db 4994 CACCTAAAGCTGGCCCAAGGACAGTCTGCAGATGATTTCTCAACAGCTTGGGAAGATT 5053
QY 4741 ATGACGAGCTGGACCCAGACAAATATGTCAGGTGTGGTTCAATAACAAAGGCTGGCAT 4800
Db 5054 ATGACGAGCTGGACCCAGACAAATATGTCAGGTGTGGTTCAATAACAAAGGCTGGCAT 5113
QY 4801 GCAATCAGCTCTTCTCCTGAATGTCAACAAATGCCATTTCTCCGGGCGCAACCTGCAAAAG 4860
Db 5114 GCAATCAGCTCTTCTCCTGAATGTCAACAAATGCCATTTCTCCGGGCGCAACCTGCAAAAG 5173
QY 4861 GGAGAGAACCCCTAGCATTATGGAATTTACTGCTTTCAATCATCCCTGAAATCTCACCAG 4920

Db 5174 GGAGAGAACCCCTAGCCATTATGGAATTAATGCTTCAATCATCCCTGAATCTCACCAG 5233
QY 4921 CAGAGCTCTCAGAGTGGCTGTATGACCAACATCAGTGGATGCTCTGTGTCCATCTGT 4980
Db 5234 CAGAGCTCTCAGAGTGGCTCCGATGACCAACATCAGTGGATGCTCTGTGTCCATCTGT 5293
QY 4981 GTACCTTTGCAATGCTCTGTCCAGCAGCTTTGTGATTCCTGATCCAGAGGG 5040
Db 5294 GTACCTTTGCAATGCTCTGTCCAGCAGCTTTGTGATTCCTGATCCAGAGGG 5353
QY 5041 GTACCAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCTACTTGGCTC 5100
Db 5354 GTACCAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCTACTTGGCTC 5413
QY 5101 TCTAATTTTGTCTGGATATGTCGAATTAAGTGTGCTCCGACACTGGTCAATATCATC 5160
Db 5414 TCTAATTTTGTCTGGATATGTCGAATTAAGTGTGCTCCGACACTGGTCAATATCATC 5473
QY 5161 TTTATCTGCTTCCAGCAGAGTCCCTATGCTCTCCACCAATCTGCCTGTCTAGCCCTT 5220
Db 5474 TTTATCTGCTTCCAGCAGAGTCCCTATGCTCTCCACCAATCTGCCTGTCTAGCCCTT 5533
QY 5221 CTACTTTTGTCTGATGCTGATGCTCAATCAGCTCTCATGTACCAGCCTCTCTTCTGTC 5280
Db 5534 CTACTTTTGTCTGATGCTGATGCTCAATCAGCTCTCATGTACCAGCCTCTCTTGTGTC 5593
QY 5281 AAGATCCCAAGCAGCTATGCTGCTGAGTGTTCACCGACAAATAGCTGAATATATCAAT 5340
Db 5594 AAGATCCCAAGCAGCTATGCTGCTGAGTGTTCACCGACAAATAGCTGAATATATCAAT 5653
QY 5341 GGCAGCTGGCACCTTTGTCTGAGTGTTCACCGACAAATAGCTGAATATATCAAT 5400
Db 5654 GGCAGCTGGCACCTTTGTCTGAGTGTTCACCGACAAATAGCTGAATATATCAAT 5713
QY 5401 GATATCTTGAAGTCCGCTTCTGATCTTCCACATTTTGCCTGGAGAGGCTCATC 5460
Db 5714 GATATCTTGAAGTCCGCTTCTGATCTTCCACATTTTGCCTGGAGAGGCTCATC 5773
QY 5461 GACATGTGAAAAACAGGCAATGGCTGATGCCCTGGAAGAGTTTGGGGAGAATCGCTTT 5520
Db 5774 GACATGTGAAAAACAGGCAATGGCTGATGCCCTGGAAGAGTTTGGGGAGAATCGCTTT 5583
QY 5521 GTGTCACCAATATCTTGGGACTTGGTGGGAGAAACCTCTTGGCCATGGCCGTGGAAGG 5580
Db 5834 GTGTCACCAATATCTTGGGACTTGGTGGGAGAAACCTCTTGGCCATGGCCGTGGAAGG 5593
QY 5581 GTGCTGTCTTCCCTCATTAATGTTCTGATCCAGTACAGATTTCTATCAGGCCACACCT 5640
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QY 5641 GTAAATGCAAGCTATCTCTCTCAATGATGAAGATGAAGATGTGAGCGCGGAAAGACAG 5700
Db 5954 GTAAATGCAAGCTATCTCTCTCAATGATGAAGATGAAGATGTGAGCGCGGAAAGACAG 6013
QY 5701 AGAATCTTGTATGTGGAGCCAGATGACATCTTAGAATCAAGGATGTGACGAGATA 5760
Db 6014 AGAATCTTGTATGTGGAGCCAGATGACATCTTAGAATCAAGGATGTGACGAGATA 6073
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Db 6074 TATAGAAGGAGCGAAGCCTGTGTGTACAGGATTTGCGTGGGCATTCCTCTCTGTGTAG 6133
QY 5821 TGCTTTGGCTCTGGAGTAAATGGGCTGGAAATCATCACTTTCAGATGTTAAAC 5880
Db 6134 TGCTTTGGCTCTGGAGTAAATGGGCTGGAAATCATCACTTTCAGATGTTAAAC 6193
QY 5881 GGAGATACCACTGTATACAGAGGAGATGCTTTCTTAAACAAAAATAGTATCTTATCAAC 5940
Db 6194 GGAGATACCACTGTATACAGAGGAGATGCTTTCTTAAACAGAAATAGTATCTTATCAAC 6253
QY 5941 ATCCATGAAGTACATCAGACATGGGCTACTGCCCTCAGTTTGCATGCCATCAGAGCTG 6000
Db 6254 ATCCATGAAGTACATCAGACATGGGCTACTGCCCTCAGTTTGCATGCCATCAGAGCTG 6313

QY 6001 TTGACTGGAGAGAACACGCTGGAGTCTTTTGGCCCTTTTGGAGAGAGTCCCGAGAGAGAA 6060
Db 6314 TTGACTGGAGAGAGAACACGCTGGAGTCTTTTGGCCCTTTTGGAGAGAGTCCCGAGAGAGAA 6373
QY 6061 GTTGGCAAGGTTTGGTGAAGTGGGCAATTCGAAACTCGGCCCTCGTGAAGTATGAGAGAAA 6120
Db 6374 GTTGGCAAGGTTTGGTGAAGTGGGCAATTCGAAACTCGGCCCTCGTGAAGTATGAGAGAAA 6433
QY 6121 TATGCTCGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6180
Db 6434 TATGCTCGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC 6493
QY 6181 GGGGGGCTCTGTGCTGTTTCTGGATGAACCCACACAGGATGGATCCCAAGCCCGG 6240
Db 6494 GGGGGGCTCTGTGCTGTTTCTGGATGAACCCACACAGGATGGATCCCAAGCCCGG 6553
QY 6241 CGGTTCTTGGTGAATGTGCTTAAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGA 6300
Db 6554 CGGTTCTTGGTGAATGTGCTTAAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGA 6363
QY 6301 TCTCATAGTATGAAGAAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGA 6360
Db 6614 TCTCATAGTATGAAGAAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGA 6673
QY 6361 AGGTTCAAGTGGCTTGGCAGTGTCCAGATCTAAAAAATAGGTTTGGAGATGTTTATACA 6420
Db 6674 AGGTTCAAGTGGCTTGGCAGTGTCCAGATCTAAAAAATAGGTTTGGAGATGTTTATACA 6733
QY 6421 ATAGTTGTAGCAATAGCAGGCTCCAAACCGGAGCTTCAAGCCTCTCCAGATTTCTTGA 6480
Db 6734 ATAGTTGTAGCAATAGCAGGCTCCAAACCGGAGCTTCAAGCCTCTCCAGATTTCTTGA 6793
QY 6481 CTTGCATTTCTGGAAGTGTTCCTTAAAGAGAAACACCGGAGCAATGCTACAATACCACTT 6540
Db 6794 CTTGCATTTCTGGAAGTGTTCCTTAAAGAGAAACACCGGAGCAATGCTACAATACCACTT 6853
QY 6541 CCATCTTCAATATCTCTGCGCAGATATTCAGATCTCTCCAGAGCAAAAGGGA 6600
Db 6854 CCATCTTCAATATCTCTGCGCAGATATTCAGATCTCTCCAGAGCAAAAGGGA 6913
QY 6601 CTCACATAGAAGTACTCTGTTTCTCAGACAACACTTGAACAGTATTTGTGAACCTT 6660
Db 6914 CTCACATAGAAGTACTCTGTTTCTCAGACAACACTTGAACAGTATTTGTGAACCTT 6973
QY 6661 GCGAAGGCAAGTATGATGACCACTTAAAGACCTTCAATTCACACAAAACAGACA 6720
Db 6974 GCGAAGGCAAGTATGATGACCACTTAAAGACCTTCAATTCACACAAAACAGACA 7033
QY 6721 GTAGTGGAGCTTGCAGTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 6780
Db 7034 GTAGTGGAGCTTGCAGTCTCAGATCTTTTCTACAGGATGAGAAAGTGAAGAAAGCTAT 7093
QY 6781 GTAT 6784
Db 7094 GTAT 7097

RESULT 15

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; Sequence 123, Application US/09984827
; Publication No. US20030056234A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, PATRICE
; APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
; APPLICANT: ARNOULD-REGUIGNE, ISABELLE
; APPLICANT: DUVERGER, NICOLAS
; APPLICANT: CAMBIEN, FRANCOIS
; TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCA1 GENE, THEIR USES, AND
; FILE REFERENCE: 03806.0522-00000
; CURRENT APPLICATION NUMBER: US/09/984.827
; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: 60/254,108
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: FR 00/14037
 ; PRIOR FILING DATE: 2000-10-31
 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 123
 ; LENGTH: 9870
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: modified_base
 ; LOCATION: (7138)
 ; OTHER INFORMATION: a, t, c or g
 US-09-984-827-123

Query Match 99.7%; Score 6764.8; DB 9; Length 9870;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 6772; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy	1	ATGGCTGTGGCCCTCAGCTGAGGTGCTGCTGGAGAACTCCTACATTCAGAGAAGA	60
Db	314	ATGGCTGTGGCCCTCAGCTGAGGTGCTGCTGGAGAACTCCTACATTCAGAGAAGA	373
Qy	61	CAACATGTCAGCTGTTACTGGAAGTGGCTGCTCTATTTATCTTCTGATCTCTGATC	120
Db	374	CAACATGTCAGCTGCTGGAAGTGGCTGCTCTATTTATCTTCTGATCTCTGATC	433
Qy	121	TCGTTCGCTGAGCTACCCACCTATGAACAAATGAATGCCATTTCCAAATAAGGC	180
Db	434	TCGTTCGCTGAGCTACCCACCTATGAACAAATGAATGCCATTTCCAAATAAGGC	493
Qy	181	ATGGCCCTGCAAGAACACTTCCTTGGGTTACGGGATTTATCTGTAATGCCAACACCC	240
Db	494	ATGGCCCTGCAAGAACACTTCCTTGGGTTACGGGATTTATCTGTAATGCCAACACCC	553
Qy	241	TGTTCCGTTACCGACTCCTGGGAGGCTCCCGAGTTGTTGGAACTTTAACAAATCC	300
Db	554	TGTTCCGTTACCGACTCCTGGGAGGCTCCCGAGTTGTTGGAACTTTAACAAATCC	613
Qy	301	ATTGGCTCGCTGTTCTCAGATGCTCGAGGCTTCTTTTATACAGCCAGAAAGACCC	360
Db	614	ATTGGCTCGCTGTTCTCAGATGCTCGAGGCTTCTTTTATACAGCCAGAAAGACCC	673
Qy	361	AGCATGAAGGACATGGGCAAACTTTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA	420
Db	674	AGCATGAAGGACATGGGCAAACTTTGAGAACATTACAGCAGATCAAGAAATCCAGCTCA	733
Qy	421	AACTTGAAGCTCAAGATTCTCTGGTGGACATGAACCTTCTCTGGGTTCTATATCAC	480
Db	734	AACTTGAAGCTCAAGATTCTCTGGTGGACATGAACCTTCTCTGGGTTCTATATCAC	793
Qy	481	AACTTCTCTCTCCAAAGTCTACTGTGACAAAGATGCTGAGGCTGATCTCTCCAC	540
Db	794	AACTTCTCTCTCCAAAGTCTACTGTGACAAAGATGCTGAGGCTGATCTCTCCAC	853
Qy	541	AGGTAATTTTGAAGGCTACCAATGATCTGACAAAGTCTGACAAAGTCTGACAAATCA	600
Db	854	AGGTAATTTTGAAGGCTACCAATGATCTGACAAAGTCTGACAAAGTCTGACAAATCA	913
Qy	601	GAAGAGATGATCAACTTGGTGACCAAGAAAGTTTCTGAGCTTTGTCCTACCAAGGAG	660
Db	914	GAAGAGATGATCAACTTGGTGACCAAGAAAGTTTCTGAGCTTTGTCCTACCAAGGAG	973
Qy	661	AACTGGCTGACAGAGGAGTACTTCGTTCCACATGGACATCTGAAAGCAATCTCTG	720
Db	974	AACTGGCTGACAGAGGAGTACTTCGTTCCACATGGACATCTGAAAGCAATCTCTG	1033
Qy	721	AGAACACTAACTCTACATCTCCCTCCGAGCAGAGGAGCTGGCTGAAGCCCAAAACA	780
Db	1034	AGAACACTAACTCTACATCTCCCTCCGAGCAGAGGAGCTGGCTGAAGCCCAAAACA	1093
Qy	781	TTGCTGCATAGTCTTGGGACTCTGGCCAGAGGCTGTTCCAGCATGAGAAAGCTTGGAGTGAC	840

Db	1094	TTGCTGCATAGTCTTGGGACTCTGCCAGAGAGTGTTCAGCATGAGAAGCTGAGTGAC	1153
Qy	841	ATGGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCAATC	900
Db	1154	ATGGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCTCCACCAATC	1213
Qy	901	TACCAGGCTGTCTCTGATGTTTCTGCGGATCCCGAGGAGGGGGCTGAAATCAAG	960
Db	1214	TACCAGGCTGTCTCTGATGTTTCTGCGGATCCCGAGGAGGGGGCTGAAATCAAG	1273
Qy	961	TCTCTCAACTGTTATGAGGACAACTTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1020
Db	1274	TCTCTCAACTGTTATGAGGACAACTTACAAAGCCCTCTTTGGAGGCAATGGCACTGAG	1333
Qy	1021	GAGATGCTGAAACCTTCTATGACAACTCTACAACCTCTTACTGCAATGATTTGATGAAG	1080
Db	1334	GAGATGCTGAAACCTTCTATGACAACTCTACAACCTCTTACTGCAATGATTTGATGAAG	1393
Qy	1081	AATTTGGAGTCTAGTCCCTCTTCCCGATTTATCTGGAAGCTCTGAGCCCTCTCGTT	1140
Db	1394	AATTTGGAGTCTAGTCCCTCTTCCCGATTTATCTGGAAGCTCTGAGCCCTCTCGTT	1453
Qy	1141	GGGAGATCTCTGTATACACCTGACACTCCAGCCACAAAGGAGGTCATGGCTGAGTGAAC	1200
Db	1454	GGGAGATCTCTGTATACACCTGACACTCCAGCCACAAAGGAGGTCATGGCTGAGTGAAC	1513
Qy	1201	AAGACCTTCCAGGAGTGGCTGTCTTCCATGATCTGAGGCAATGGGAGGAGTCTCAGC	1260
Db	1514	AAGACCTTCCAGGAGTGGCTGTCTTCCATGATCTGAGGCAATGGGAGGAGTCTCAGC	1573
Qy	1261	CCCAGATCTCGAGCTTTCATGGAGAACAGCCAAAGAAATGAGACCTTGTCCGATGCTGTG	1320
Db	1574	CCCAGATCTCGAGCTTTCATGGAGAACAGCCAAAGAAATGAGACCTTGTCCGATGCTGTG	1633
Qy	1321	GACAGCGGACAAATGACCACTTTTGGGAACAGAGTTGGATGGCTTAGATTTGACAGCC	1380
Db	1634	GACAGCGGACAAATGACCACTTTTGGGAACAGAGTTGGATGGCTTAGATTTGACAGCC	1693
Qy	1381	CAAGACATCTGGGCTTTTGGCCAAAGCAGCAGAGGATGTCAGTCCAGTAATGGTCT	1440
Db	1694	CAAGACATCTGGGCTTTTGGCCAAAGCAGCAGAGGATGTCAGTCCAGTAATGGTCT	1753
Qy	1441	GTGTACACCTGGAGAGAGCTTTTCAACGAGACTTAACAGGCAATCCGACCACTATCTGC	1500
Db	1754	GTGTACACCTGGAGAGAGCTTTTCAACGAGACTTAACAGGCAATCCGACCACTATCTGC	1813
Qy	1501	TTTATGGAGTGTCAACCTTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC	1560
Db	1814	TTTATGGAGTGTCAACCTTGAACAGCTAGAACCCATAGCAACAGAGTCTGGCTCATC	1873
Qy	1561	AACAACTCCATGGAGCTCTGATGAGAGGAGTTCTGGGCTGGTATTGTTCACATGGA	1620
Db	1874	AACAACTCCATGGAGCTCTGATGAGAGGAGTTCTGGGCTGGTATTGTTCACATGGA	1933
Qy	1621	ATTACTCCAGCAGCATTTGAGTCCCATCATGTCAGTCAAGTACAGATCCGATGGACATT	1680
Db	1934	ATTACTCCAGCAGCATTTGAGTCCCATCATGTCAGTCAAGTACAGATCCGATGGACATT	1993
Qy	1681	GACAACTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGACCTTGGCTCGAGCT	1740
Db	1994	GACAACTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGACCTTGGCTCGAGCT	2053
Qy	1741	GACCCCTTTGAGGACATCGGTACGCTGCGGGGCTTCCGCTTACTTCAGAGATGTTGTG	1800
Db	2054	GACCCCTTTGAGGACATCGGTACGCTGCGGGGCTTCCGCTTACTTCAGAGATGTTGTG	2113
Qy	1801	GAGCAGGCAATCATCAGGCTGCTGACGGGACCCGAGAGAAACCTGTTGTCTATATGAA	1860
Db	2114	GAGCAGGCAATCATCAGGCTGCTGACGGGACCCGAGAGAAACCTGTTGTCTATATGAA	2173
Qy	1861	CAGATCCCTATCCCTGTTTACGTTGATGACATCTTCTTCGGGCTGATGAGCCGTTCAATG	1920

Db 2174 CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGTGATGAGCGGTCAATG 2233
QY 1921 CCCCTCTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCAATCGTG 1980
Db 2234 CCCCTCTTCATGACGCTGGCCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCAATCGTG 2293
QY 1981 TATGAGAAGGAGCGACGGCTGAAAGAGACCATGCGGATCATGGGCTGCACAAACAGCATA 2040
Db 2294 TATGAGAAGGAGCGACGGCTGAAAGAGACCATGCGGATCATGGGCTGCACAAACAGCATA 2353
QY 2041 CTCCTGTTTAGCTGGTTCAATAGTAGCTCATCTCTTCCTTGTGAGCGCTGGCCCTGCTA 2100
Db 2354 CTCCTGTTTAGCTGGTTCAATAGTAGCTCATCTCTTCCTTGTGAGCGCTGGCCCTGCTA 2413
QY 2101 GTGGTCATCCTGAAGTTAGGAACCTGCTGCCCTACAGTGATCCAGCGTGGTGTTC 2160
Db 2414 GTGGTCATCCTGAAGTTAGGAACCTGCTGCCCTACAGTGATCCAGCGTGGTGTTC 2473
QY 2161 TTCCTGTCGCTGTTTCTGTGTGTGACAAATCCCTGCACTGCTTCCCTGATTAGCACACTTTC 2220
Db 2474 TTCCTGTCGCTGTTTCTGTGTGTGACAAATCCCTGCACTGCTTCCCTGATTAGCACACTTTC 2533
QY 2221 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCATCTACTTACGCTGTACCTGGCC 2280
Db 2534 TCCAGAGCAACCTGGCAGCAGCTGTGGGGCATCATCTACTTACGCTGTACCTGGCC 2593
QY 2281 TACGTCCTGTGTGTGGCATGGCAGGACTACGTTGGGCTTACACTCAAGATCTTCCCTAGC 2340
Db 2594 TACGTCCTGTGTGTGGCATGGCAGGACTACGTTGGGCTTACACTCAAGATCTTCCCTAGC 2653
QY 2341 CTGCTGTCTCCTGTGGCTTTGGGTTGGCTGTGAGTACTTTGCCCTTTTGTAGAGAGAG 2400
Db 2654 CTGCTGTCTCCTGTGGCTTTGGGTTGGCTGTGAGTACTTTGGCCCTTTTGTAGAGAGAG 2713
QY 2401 GGCATTGGAGTGCAGTGGGCAACCTGTTTGGAGTCTCTGTGGAGGAAGATGGCTTCAAT 2460
Db 2714 GGCATTGGAGTGCAGTGGGCAACCTGTTTGGAGTCTCTGTGGAGGAAGATGGCTTCAAT 2773
QY 2461 CTCACCACTTCAGTCTCATGATGCTGTTTGACACCTTCTCTATGAGGGGTGATGACCTGG 2520
Db 2774 CTCACCACTTCGGTCTCATGATGCTGTTTGACACCTTCTCTATGAGGGGTGATGACCTGG 2833
QY 2521 TACATTGAGGCTGTCTTCCAGGCGCAGTACGGAATTCGCCAGCCCTGGTATTTTCCCTTGC 2580
Db 2834 TACATTGAGGCTGTCTTCCAGGCGCAGTACGGAATTCGCCAGCCCTGGTATTTTCCCTTGC 2893
QY 2581 ACCAAGTCTACTGTTTGGCGAGAAAGTGTGATGAGAGAGCCACCTGGTGTCCAAACAG 2640
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QY 2641 AAGAGAATGTCAAGAAATCTGATGAGGAGGAACCCACCCACTTGAAGCTGGCGGTGTC 2700
Db 2954 AAGAGAATGTCAAGAAATCTGATGAGGAGGAACCCACCCACTTGAAGCTGGCGGTGTC 3013
QY 2701 ATTCAAGACCTGGTAAAAGTCTACCGAGATGGGATGGAAGTGGCTGTGCGATGGCCTGGCA 2760
Db 3014 ATTCAAGACCTGGTAAAAGTCTACCGAGATGGGATGGAAGTGGCTGTGCGATGGCCTGGCA 3073
QY 2761 CTGAATTTTATGAGGGCCAGATCACCTCCCTCTGCGGCCACAATGGAGCGGGGAAGAGC 2820
Db 3074 CTGAATTTTATGAGGGCCAGATCACCTCCCTCTGCGGCCACAATGGAGCGGGGAAGAGC 3133
QY 2821 ACCACCATGTCAATCCTGACCGGGTGTGTCCCGCCGACCTCGGCGACCGCTACATCCTG 2880
Db 3134 ACCACCATGTCAATCCTGACCGGGTGTGTCCCGCCGACCTCGGCGACCGCTACATCCTG 3193
QY 2881 GGAAAGACATTCGCTCTGAGATGAGCAACCATCCGGGAGACCTTGGGGGTCTGTCCCGAG 2940
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QY 2941 CATAACGTGCTGTTTGACATGCTGACTGTGGAAGAACACATCTGGTCTATGCGCCGCTTG 3000
Db 3254 CATAACGTGCTGTTTGACATGCTGACTGTGGAAGAACACATCTGGTCTATGCGCCGCTTG 3313

QY 3001 AAAGGGCTCTCTGAGAACGACGCTGAAGCGGAGATGAGCAGATGGCCCTGGATGTGGT 3060
Db 3314 AAAGGGCTCTCTGAGAACGACGCTGAAGCGGAGATGAGCAGATGGCCCTGGATGTGGT 3373
QY 3061 TTGCATCTCAAGCAAGCTGAAAAGCAAAACCAAGCAGCTGTGAGTGGTGAATGCAGAGAAAG 3120
Db 3374 TTGCATCTCAAGCAAGCTGAAAAGCAAAACCAAGCAGCTGTGAGTGGTGAATGCAGAGAAAG 3433
QY 3121 CTATCTGTGGCTTGGCCTTGTGCGGGGATCTAAGGTTGTCAATTTCTGGATGAACCCACA 3180
Db 3434 CTATCTGTGGCTTGGCCTTGTGCGGGGATCTAAGGTTGTCAATTTCTGGATGAACCCACA 3493
QY 3181 GCTCGTGTGACCCCTTACTCCCGCAGGGGAATATGGAGCTGTCTGAAATACCCACAA 3240
Db 3494 GCTCGTGTGACCCCTTACTCCCGCAGGGGAATATGGAGCTGTCTGAAATACCCACAA 3553
QY 3241 GGCGCCACCATTAATTTCTCTTACACACCATGATGAAGCGGACGCTCTGCGGGGACAG 3300
Db 3554 GGCGCCACCATTAATTTCTCTTACACACCATGATGAAGCGGACGCTCTGCGGGGACAG 3613
QY 3301 ATTGCCATCATCTCCCATGGAGAGCTGTGCTGTGGGCTCCCTCCCTGTTCTGAGAGAAC 3360
Db 3614 ATTGCCATCATCTCCCATGGAGAGCTGTGCTGTGGGCTCCCTCCCTGTTCTGAGAGAAC 3673
QY 3361 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGAAATCCTCCCTCAGT 3420
Db 3674 CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGAAATCCTCCCTCAGT 3733
QY 3421 TCCTGCAAGAACAGTAGTAGCAGCTGTGCTACTTCTGAAAAGAGGACAGTGTTCCTCAG 3480
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Db 3794 AGCAGTTCTGATGTGCTGGCCTGGCAGGACCATGAGAGTGCACACGCTGACCTCGATGTC 3853
QY 3541 TCCTGATCTCCAACTTCATCAGGAAGCATGTGCTGAAGCCCGGCTGTGGGAAGACATA 3600
Db 3854 TCCTGATCTCCAACTTCATCAGGAAGCATGTGCTGAAGCCCGGCTGTGGGAAGACATA 3913
QY 3601 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGTGCCTAAGGAGGAGGCTTTGTGGAA 3660
Db 3914 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGTGCCTAAGGAGGAGGCTTTGTGGAA 3973
QY 3661 CTCTTTTCATGAGATGTGATGACCGCTCTCAGACCTGGGCAATTTCTAGTTATGCACTCTCA 3720
Db 3974 CTCTTTTCATGAGATGTGATGACCGCTCTCAGACCTGGGCAATTTCTAGTTATGCACTCTCA 4033
QY 3721 GAGACGACCTTGAAGAAATATTTCTCAAGTGGCGGAGAGAGTGGGTGGATGCTGAG 3780
Db 4034 GAGACGACCTTGAAGAAATATTTCTCAAGTGGCGGAGAGAGTGGGTGGATGCTGAG 4093
QY 3781 ACCTCAGATGGTACCTTGCACGACGACAAACAGCGCGGCTTCGCGGACAGCAGAGC 3840
Db 4094 ACCTCAGATGGTACCTTGCACGACGACAAACAGCGCGGCTTCGCGGACAGCAGAGC 4153
QY 3841 TGTCTTGCCTGCTCACTGAAGATGATGCTGTGATCTCCAAATGATTTCTGACATAGACCA 3900
Db 4154 TGTCTTGCCTGCTCACTGAAGATGATGCTGTGATCTCCAAATGATTTCTGACATAGACCA 4213
QY 3901 GAATCCAGAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAGGGTCCCTACCAGGTGAAA 3960
Db 4214 GAATCCAGAGAGACAGACTTGTCTCAGTGGGATGGATGGCAAGGGTCCCTACCAGGTGAAA 4273
QY 3961 GCGTGGAACTTACAGACGACAGTGTGGCCCTTTTGTGGAGAGACTGCTTAATGCC 4020
Db 4274 GCGTGGAACTTACAGACGACAGTGTGGCCCTTTTGTGGAGAGACTGCTTAATGCC 4333
QY 4021 AGACGAGTCCGAAAGGATTTTTTGTCTGATGCTGTGCTGACGCTGTGTTGCTGCAAT 4080
Db 4334 AGACGAGTCCGAAAGGATTTTTTGTCTGATGCTGTGCTGACGCTGTGTTGCTGCAAT 4393

Qy	4081	GCCTTGTGTTCAGCCTGATGCTGCCACCCCTTTGGCAAGTACCCAGCCTGGAACTTCAG	4144
Db	4394	GCCTTGTGTTCAGCCTGATGCTGCCACCCCTTTGGCAAGTACCCAGCCTGGAACTTCAG	4453
Qy	4141	CCCTGGATGTACAACGAACAGTACACATTTGTACGAATGATGCTCTGAGGACACGGGA	4200
Db	4454	CCCTGGATGTACAACGAACAGTACACATTTGTACGAATGATGCTCTGAGGACACGGGA	4513
Qy	4201	ACCTTGGAACTCTTAAACGCCCTCACCAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4260
Db	4514	ACCTTGGAACTCTTAAACGCCCTCACCAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA	4573
Qy	4261	GGAAACCCCAATCCAGACACGCCCTGCCAGCGAGGGGAGAGTGGACCACTGCCCCA	4320
Db	4574	GGAAACCCCAATCCAGACACGCCCTGCCAGCGAGGGGAGAGTGGACCACTGCCCCA	4633
Qy	4321	GTTCGCCAGACCATCATGACCTCTTCCAGAATGGAACTGGACAATCCAGAACCCCTTCA	4380
Db	4634	GTTCGCCAGACCATCATGACCTCTTCCAGAATGGAACTGGACAATCCAGAACCCCTTCA	4693
Qy	4381	CTTGCATGCCAGTGTAGACGCACAAAATCAAGAAGATGCTGCTGTGTCTCCCCAGGG	4440
Db	4694	CTTGCATGCCAGTGTAGACGCACAAAATCAAGAAGATGCTGCTGTGTCTCCCCAGGG	4753
Qy	4441	GCAGGGGGCTGCTCCTCCCAAGAAACAAAACACTGCAGATATCCTTTCAGGACCTG	4500
Db	4754	GCAGGGGGCTGCTCCTCCCAAGAAACAAAACACTGCAGATATCCTTTCAGGACCTG	4813
Qy	4501	ACAGGAAGAAACAATTCGGATTTATGCTGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4560
Db	4814	ACAGGAAGAAACAATTCGGATTTATGCTGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4873
Qy	4561	TTAAAGAACAAAGATCTGGTGAATGAGTTTAGTATGGCGCTTTTCCCTGGGTGTCAGT	4620
Db	4874	TTAAAGAACAAAGATCTGGTGAATGAGTTTAGTATGGCGCTTTTCCCTGGGTGTCAGT	4933
Qy	4621	AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAA	4680
Db	4934	AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCATCAACAAATGAAGAAA	4993
Qy	4681	CACCTAAAGCTGCCAAGCACAGTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	4740
Db	4994	CACCTAAAGCTGCCAAGCACAGTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTT	5053
Qy	4741	ATGACAGGACTGGACACCAGAAATATGTCAGGTGTGGTTTCAATAACAAGGGCTGGCAT	4800
Db	5054	ATGACAGGACTGGACACCAGAAATATGTCAGGTGTGGTTTCAATAACAAGGGCTGGCAT	5113
Qy	4801	GCAATCAGCTCTTCTCGAATGTCATCAACATGCCATTCCTCCGGGCCCAACCTGCRAAG	4860
Db	5114	GCAATCAGCTCTTCTCGAATGTCATCAACATGCCATTCCTCCGGGCCCAACCTGCRAAG	5173
Qy	4861	GGAGAAACCCCTAGCCATTATGGAATTAAGTGTTCATATCCCTGAACTCATCCCAAG	4920
Db	5174	GGAGAAACCCCTAGCCATTATGGAATTAAGTGTTCATATCCCTGAACTCATCCCAAG	5233
Qy	4921	CAGCAGCTCTCAGAGTGGCTGTGATGACCACATCAGTGGATGTCTTGTGTCATCTGT	4980
Db	5234	CAGCAGCTCTCAGAGTGGCTGTGATGACCACATCAGTGGATGTCTTGTGTCATCTGT	5293
Qy	4981	GTCACTTTTTCGAATGTCCCTGTCGCCAGCCAGCTTTGTCGTTATTCCTGATCCAGGACGG	5040
Db	5294	GTCACTTTTTCGAATGTCCCTGTCGCCAGCCAGCTTTGTCGTTATTCCTGATCCAGGACGG	5353
Qy	5041	GTGACAAAGCAAAACACCTGCGATTCATCAGTGGAGTGAAGCCGTGCACTACTGGCTC	5100
Db	5354	GTGACAAAGCAAAACACCTGCGATTCATCAGTGGAGTGAAGCCGTGCACTACTGGCTC	5413
Qy	5101	TCTAAATTTTGTCTGGGATATGTGCAATTAAGTGTGTCCTGCCACACTGGTCATTAATCATC	5160
Db	5414	TCTAAATTTTGTCTGGGATATGTGCAATTAAGTGTGTCCTGCCACACTGGTCATTAATCATC	5473
Qy	5161	TTCACTGTCTTCAGCAGGAAGCTCTATGTGCTCTCCACCAATCTGCCTGTGCTAGCCCTT	5220

Db	5474	TTCACTGCTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTCTAGCCCTT	5533
Qy	5221	CTACTTTTGTGTATGGGTGGTCAATCACACACTCTCATGTACCCAGCCTCTCTTGTGTTC	5280
Db	5534	CTACTTTTGTGTATGGGTGGTCAATCACACACTCTCATGTACCCAGCCTCTCTTGTGTTC	5593
Qy	5281	AAGATCCCCAGCAGACCTAATGTGTGTCTACACGGGTGAACCTCTTCATTGGCATTAAT	5340
Db	5594	AAGATCCCCAGCAGACCTAATGTGTGTCTACACGGGTGAACCTCTTCATTGGCATTAAT	5653
Qy	5341	GGCAGCTGGCCACCTTTGTGTGTGGAGCTGTTCACCGACAATAGCTGAATAATATCAAT	5400
Db	5654	GGCAGCTGGCCACCTTTGTGTGTGGAGCTGTTCACCGACAATAGCTGAATAATATCAAT	5713
Qy	5401	GATATCTGAAGTCCGTGTCTTGATCTTCCACATATTTTGCCCTGGGAGAGGCTCATC	5460
Db	5714	GATATCTGAAGTCCGTGTCTTGATCTTCCACATATTTTGCCCTGGGAGAGGCTCATC	5773
Qy	5461	GACATGTGAAACACAGCAATGGCTGATGCCCTGGGAAGGTTTGGGAGAATCGCTTT	5520
Db	5774	GACATGTGAAACACAGCAATGGCTGATGCCCTGGGAAGGTTTGGGAGAATCGCTTT	5833
Qy	5521	GTGTACCAATATCTTTGGGACTTTGGTGGACGAAACCTCTTCGCCATGCCCTGGAAGG	5580
Db	5834	GTGTACCAATATCTTTGGGACTTTGGTGGACGAAACCTCTTCGCCATGCCCTGGAAGG	5893
Qy	5581	GTGTGTCTTCTCTCAATCTGTTCTGATCCAGTACAGATCTTTCATCAGGCCCAGACCT	5640
Db	5894	GTGTGTCTTCTCTCAATCTGTTCTGATCCAGTACAGATCTTTCATCAGGCCCAGACCT	5953
Qy	5641	GTAATCGAAAGCTATCTCTCTGAATGATGAAGATGTGAGCGGGGAAAGACAG	5700
Db	5954	GTAATCGAAAGCTATCTCTCTGAATGATGAAGATGTGAGCGGGGAAAGACAG	6013
Qy	5701	AGAATCTTGATGGTGAGGCCAGATGACATCTTAGAATCAAGAGTTTGACGAAGATA	5760
Db	6014	AGAATCTTGATGGTGAGGCCAGATGACATCTTAGAATCAAGAGTTTGACGAAGATA	6073
Qy	5761	TATAGAAGGAAGCGGAAGCTGCTGTTGACAGGATTTGGCTGGCATTCCTCTGGTGAG	5820
Db	6074	TATAGAAGGAAGCGGAAGCTGCTGTTGACAGGATTTGGCTGGCATTCCTCTGGTGAG	6133
Qy	5821	TGCTTTGGGTCCTGGAGTTAATGGGCTGGAAATCAATCACTTTCAAGATGTTAACA	5880
Db	6134	TGCTTTGGGTCCTGGAGTTAATGGGCTGGAAATCAATCACTTTCAAGATGTTAACA	6193
Qy	5881	GGAGATACCACTGTTACCAGAGAGATGCTTTCCCTTACAAAAATAGTATCTTTCAAC	5940
Db	6194	GGAGATACCACTGTTACCAGAGAGATGCTTTCCCTTACAAAAATAGTATCTTTCAAC	6253
Qy	5941	ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGTATGCCATCACAGGTG	6000
Db	6254	ATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTTGTATGCCATCACAGGTG	6313
Qy	6001	TTGACTGGGAGAACACGTGGAGTCTTTGGCCCTTTTGAGAGGAGTCCACAGAAAGAA	6060
Db	6314	TTGACTGGGAGAACACGTGGAGTCTTTGGCCCTTTTGAGAGGAGTCCACAGAAAGAA	6373
Qy	6061	GTTGGCAAGGTTGTGTAGTGGGCGATTGCGAACTGGGCTCGTGAAGTATGGAGAAAA	6120
Db	6374	GTTGGCAAGGTTGTGTAGTGGGCGATTGCGAACTGGGCTCGTGAAGTATGGAGAAAA	6433
Qy	6121	TATCGTGGTAACATATAGTGAGGCACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6180
Db	6434	TATCGTGGTAACATATAGTGAGGCACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6493
Qy	6181	GGCGGGCTCTGTGTGTGTTCTTGGATGAACCCACACAGGCATGGATCCCAAGCCCGG	6240
Db	6494	GGCGGGCTCTGTGTGTGTTCTTGGATGAACCCACACAGGCATGGATCCCAAGCCCGG	6553
Qy	6241	CGGTTCTGTGGAAATGTGCCCTAAGTGTGTGTCAGAGGGGAGATCACTAGTGTCTTACA	6300

Db 6554 CGGTTCTTGTGGAATTGTGCCCTAAAGTGTGTCAAGAGGGGAGATCAGTAGTGCTTACA 6613
QY TCTCATAGTATGGAAGATGTGAAGCTCTTTGCACATAGGATGGCAATCATGTGTCATATGGA 6360
Db 6614 TCTCATAGTATGGAAGATGTGAAGCTCTTTGCACATAGGATGGCAATCATGTGTCATATGGA 6673
QY 6361 AGGTTACAGTGGCTTGGCAGTCTCCAGCATCTAAATAATAGCTTTGGAGATGGTTTATACA 6420
Db 6674 AGGTTACAGTGGCTTGGCAGTCTCCAGCATCTAAATAATAGCTTTGGAGATGGTTTATACA 6733
QY 6421 ATAGTTGTACGATAGCAGGTTCCACCGGACCTGAAGCCTGTCCAGGATTTCTTTTGA 6480
Db 6734 ATAGTTGTACGATAGCAGGTTCCACCGGACCTGAAGCCTGTCCAGGATTTCTTTTGA 6793
QY 6481 CTTGCATTTCCCTGGAGTGTCTTAAAGAGAGAAACACCGGACATGCTACAATACCAGCTT 6540
Db 6794 CTTGCATTTCCCTGGAGTGTCTTAAAGAGAGAAACACCGGACATGCTACAATACCAGCTT 6853
QY 5541 CCATCTTCATTTATCTTCTGCGCAGGATATTCAGCATCCTCTCCAGAGCAAAAAGCGA 6600
Db 6854 CCATCTTCATTTATCTTCTGCGCAGGATATTCAGCATCCTCTCCAGAGCAAAAAGCGA 6913
QY 6601 CTCCACATAGAGACTACTCTCTTTCTCAGACACACTTGACCAAGTATTTGTGAACCTT 6660
Db 6914 CTCCACATAGAGACTACTCTCTTTCTCAGACACACTTGACCAAGTATTTGTGAACCTT 6973
QY 6661 GCCAAGGACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 6720
Db 6974 GCCAAGGACCAAGTATGATGACCACTTAAAGACCTCTCATTTACACAAAACAGACA 7033
QY 6721 GTAGTGGAGTTGGCAGTTCTCAGTCTTTCTCAGAGGATGAGAAAGTCAAAAGAGCTAT 6780
Db 7034 GTAGTGGAGTTGGCAGTTCTCAGTCTTTCTCAGAGGATGAGAAAGTCAAAAGAGCTAT 7093
QY 6781 GTAT 6784
Db 7094 GTAT 7097

Search completed: April 4, 2003, 06:45:44
Job time : 505.143 secs

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2003, 09:40:44 ; Search time 7668.53 Seconds
(without alignments)
14327.411 Million cell updates/sec

Title: US-09-595-526c-l_COPY_291_7074

Perfect score: 6784
Sequence: 1 atgctttgttgccctcagct.....agtgaagaagaactatgtat 6784

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: em_esta:*
- 2: em_estum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_estl:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pln:*
- 21: em_gss_vit:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	692.4	10.2	809	13	BI754756
2	639.8	9.4	834	13	BI854140
3	543.6	8.0	837	12	BF160011
4	536.8	7.9	652	10	BB468374
5	532.4	7.8	724	13	BG202023
6	526.6	7.8	720	13	BI248317

7	508.2	7.5	702	13	BI658600
8	483.6	7.1	1004	11	BC034824
9	474.6	7.0	878	13	BI182779
10	473	7.0	562	10	BE65489
11	459.4	6.8	515	12	BF04524
12	447.6	6.6	554	12	BF076322
13	433.2	6.4	518	12	BF042703
14	428.8	6.3	463	12	BE175104
15	425.4	6.3	427	13	BM153383
16	424.2	6.3	998	12	RG678861
17	411	6.1	596	9	AA063753
18	399.2	5.9	417	10	AA362709
19	366.2	5.4	412	10	AW380897
20	365.8	5.4	441	12	BF042938
21	364.6	5.4	662	13	BI468033
22	363.6	5.4	434	10	AW322690
23	362	5.3	422	12	BE929660
24	345.6	5.1	366	12	BF951740
25	340.8	5.0	717	12	BE742059
26	337	5.0	835	10	AW013420
27	327.6	4.8	351	12	BF928185
28	325.8	4.8	623	10	AW421371
29	321.2	4.7	352	12	BF892148
30	320.8	4.7	324	10	AW845151
31	318.8	4.7	736	9	AU135588
32	318.2	4.7	2640	11	U66891
33	315.6	4.7	551	9	AI733552
34	312.2	4.6	591	9	AL588915
35	309.2	4.6	782	12	BG775975
36	309	4.6	641	14	BQ637544
37	308.8	4.6	381	12	BE757461
38	301.4	4.4	786	13	BI736551
39	301.2	4.4	699	13	BI735256
40	299	4.4	363	10	AV647223
41	296.4	4.4	359	10	BB871492
42	288	4.4	743	14	BQ442860
43	286.2	4.2	549	13	BI976880
44	286.2	4.2	603	14	BM722367
45	285.4	4.2	529	12	BG883616

ALIGNMENTS

RESULT 1
BI754756
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BI754756 809 bp mRNA linear EST 25-SEP-2001
603025477F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:519595 5',
mRNA sequence.
BI754756.1 GI:15746334
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 809)
NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1490 row: i column: 20
High quality sequence stop: 768.

FEATURES
Source
1. .809
Location/Qualifiers

10

10

/note="Organ: lung; Vector: PCMV-SPORT6; Site.1: SalI; Site.2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"					
BASE COUNT	226 a	188 c	230 g	193 t	
ORIGIN					
	Query Match	8.0%;	Score 543.6;	DB 12;	Length 837;
	Best Local Similarity	88.4%;	Pred. No. 1e-137;		
	Matches 647;	Conservative	0;	Mismatches 79;	Indels 6;
	Gaps				
QY	5963	TGGGCTACTGCCCTCAGTTTGATGTCACACAGAGCTGTGTA	CTGGGAGAGAACACACGTGG	6022	
Db	13	TGGGCTACTGCCCTCAGTTTGCGCGGCATCACAGAGCTGTG	ACTCTGGAAGAGCATGTGG	72	
QY	6023	AGTTCCTTTGCCCTTTTG - AGAGAGTCCAGAGAAGAGTT	GGCAAGSTGGTGAGTGG	6081	
Db	73	AGTTCCTTTGCCCTTTTGAGGGNGTCCCAGAAAAGGAGATT	GGCAAGSTGGTGAAATGG	132	
QY	6082	GGCATTCGGAACATGGGCTCTGTAAGTATGAGAAAAAATA	TGCTGGTAACATATATGGA	6141	
Db	133	GCAATTGCGAAACATGGGCTCTGTAAGTATGAGAAAAAATA	TGCTGGTAACATATACAGTGGC	192	
QY	6142	GGCAACAACAGCAAGCTCTCTACAGGCATGGCTTTGAT	CGGGGGCCCTCTGTGGTGTT	6201	
Db	193	GGCAACAACAGCAAGCTCTCCACAGCCATGGCTTTGATT	GGCGGCCCTCTGTGGTGTT	252	
QY	6202	CTGGATGAACCACACACAGCATGGATCCCAAGCCCCGGG	TCTTCTGTGAAATGTGCC	6261	
Db	253	CTGGATGAACCACACAGCATGGATCCCAAGCCCCGGGAT	TCTTCTGTGAA - TGTGCC	311	
QY	6262	CTAAGTGTCTCAAGGAGGGAGATCAGTAGTGCCTTACAT	CATCATAGTATGGAAGATGT	6321	
Db	312	CTAAG - CATGTC AAGGAGGGAGATCTGTAGTCCCTT	ACATCTCATAGTATGGAAGATGT	370	
QY	6322	GAAGCTCTTTGCACTAGGATGGCAATCGTCAATGGNAG	TTTCAGTGGCTTGGCAGT	6381	
Db	371	GAAGCTCTTTGTACAAGATGGGCCAATATGGTCAATGG	AAGGTTTCAGTGGCTTGGCAGT	430	
QY	6382	GTCACGATCTAAATAATAGTTTGAGAGATGGTTATACA	ATAGTTGTACGAATAGCAGG	6441	
Db	431	GTCCAACATCTGAAAACAGGTTTGAGATGGTTATACA	ATAGTTGTACGAATAGCAGC	490	
QY	6442	TCCNAACCGGACCTGAAGCCTGTCCAGGATTTCTTTG	NCTTCGATTTCTTGGAGTGT	6501	
Db	491	TCCNAACCGTCACTGAAGCCTGTCCAGGAGTTCCTTT	GGAGTTCGATTTCCAGGAAGTCT	550	
QY	6502	CTAAAGAGAAACACCGGAACATGCTTACAAATACCA	AGCTTCCATCTTCATCTCTCTG	6561	
Db	551	CTAAAGAGAAACATCGMAACATGCTTCAGTACCAG	CTCCATCTCTCTCTCTCTCTA	610	
QY	6562	GCAGAGATATCAGATCTCTCCAGAGCAAAGCGACT	CCACA - TAGAGACTACTC	6620	
Db	611	GCAGAGATATCAGATCTCTCCAGAGCAAAGCGACT	CCACATTAGAAGACTACTC	670	
QY	6621	TGTTTCTCAGACAACACTTGACCAAGTATTTTGAA	CTTTTGGCAAGCTTGGCAAGGCCAAAGTATGA	6680	
Db	671	TGTTTCTCAGACAACACTTGACCAAGTATTT - GT	GAACTTTGGCAAGGCCAAAGTATGA	728	
QY	6681	TGACCACTTTAAA	6692		
Db	729	TTGNCCCTTAAA	740		
RESULT 4					
BB468374					
LOCUS	BB468374	RIKEN full-length enriched, 12 days embryo eyeball Mus	musculus cDNA clone D230019D04 3' similar to X75926 M.musculus abd	linear	EST 25-OCT-2000
DEFINITION					
name					

[illegible]

SOURCE	mus musculus	cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 652)	GAGAGAGATTCGAGTTAATAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1."
REFERENCE	Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, P., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Tanahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.	BASE COUNT 151 a 182 c 179 g 140 t
AUTHORS	RIKEN Mouse ESTs (Arakawa, T., et al. 2001)	ORIGIN
TITLE	Unpublished (2001)	Query Match 7.98; Score 536.8; DB 10; Length 652;
JOURNAL	On Jul 22, 2000 this sequence version replaced gi:9385563.	Best Local Similarity 89.08; Pred. No. 6.1e-136;
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamakata, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Location/Qualifiers 1. .652 /organism="Mus musculus" /db_xref="taxon:10090" /clone="D230019D04" /clone_lib="RIKEN full-length enriched, 12 days embryo eyeball" /tissue_type="eyeball" /dev_stage="12 days embryo" /lab_host="DH10B" /note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by	Matches 580; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
		QY 3811 AACAGCGCGCTTCGGGCAACAGCAGCTCTCTGCCCGCTTCACTGAAGATGATGCT 3870
		DB 1 AACAGCGGGCTTCGGGGCAACAGCAGCTCTCTGCCCGCTTCACTGAAGATGATGCT 60
		QY 3871 GCTGATCCAAATGATTTGATAGATAGACCCAGAAATCCAGAGAGAGACTTGTCTCAGTGGG 3930
		DB 61 GTTGATCCAAATGATTTGATAGATAGACCCAGAAATCCAGAGAGAGACTTGTCTCAGTGGG 120
		QY 3931 ATGGATGCAAGAGGCTCTACAGGTGAAGGCTGGAACTTACACAGCAGACAGTTTGTG 3990
		DB 121 ATGACGGCAAGGCTCTACAGGTGAAGGCTGGAACTTACACAGCAGACAGTTTGTG 180
		QY 3991 GCCCTTTTGTGGAAGAGACTCTAATTCGCCAGCGAGTCCGGAAGAGTTTGTGCTCAG 4050
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		DB 241 ATTGTCTTGCAGCTGTGTTTGTCTGATTCGCTCCCTTGTGTCAGCTGATGTCGTCACCC 300
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		DB 301 TTTGCAAGTACCCAGCTCGAACTTCAGCCCTGGATGTACAAACAGACAGTACACATTT 360
		QY 4171 GTCAGCAATGATGCTCTGAGAGACACGGGAACTTGAAGTCTTAAACGCCCTCACCAAA 4230
		DB 361 GTCAGTAAATGATGCTCTGAGAGACACGGGAACTTGAAGTCTTAAACGCCCTCACCAAA 420
		QY 4231 GACCTGTGCTTGGGACCCGCTGTATGGAAGAAACCAATCCAGACACGCCCTGCCAG 4290
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		QY 4291 GCAGGGAGAGAGTGGACCACTGCCCGCTTCCAGAGACCATCATGGACCTTCCAG 4350
		DB 481 GCTGGGAGAGAGTGGACCACTGCCCGCTTCCAGAGACCATCATGGACCTTCCAG 540
		QY 4351 AATGGAACTGGCAATTCAGAACCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4410
		DB 541 AATGGAACTGGCAATTCAGAACCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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RESULT 5		
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DEFINITION	602822304f1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4951320 5', mRNA sequence.	724 bp mrna linear EST 05-JUN-2001
ACCESSION	BG920223	
VERSION	BG920223.1	GI:14300699
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 724)	
AUTHORS	NTH-MGC http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10907 row: g column: 01
High quality sequence stop: 631.

FEATURES
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BASE COUNT 198 a 179 c 178 g 168 t

ORIGIN

Query Match 7.8%; Score 532.4; DB 13; Length 724;
Best Local Similarity 88.2%; Pred. No. 1.1e-134;
Matches 636; Conservative 0; Mismatches 77; Indels 8; Gaps 5;

QY 6021 GGAGTCTTTCCTTTGAGAGAGTCCAGACAGAAAGTTGGCAAGTTGGTGNATG 6080
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QY 6081 GGCGATTTCGGAAGTGGCCCTCTGAAAGTATGGAGAAATATGCTGTAACATAGTGG 6140
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Db 61 GGCAATTCGCAAACTGGCCCTGGTAAAGTATGGAGAAATATGCCAGTAACATAGTGG 120
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QY 6141 AGGCAACAGCGAAGTCTCTACAGCATGGCTTTGATCGGGGGCTCC-TGTGGTGT 6199
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Db 121 CGGCAACAGAAAGTCTCCAGAGCATGGCTTTGATTCGGGAGCTCCATGTTGGTGT 180
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QY 6200 TTCGTGATGAACCCACACAGGATGATCCAAAGCCGGCTTTGTTGGAAATGTG 6259
|||||
Db 181 TTCTGGATGAACCAACACAGGATGACCCCTAAAGCCGGAGATCTCTGGAAATGTG 240
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QY 6260 CCTTAAGTGTTCAGAGGGGAGATCAGTAGTGCTTACATCTCATAGTATGGAAGAT 6319
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Db 241 CCTTAAGCATGTCAAGGGGGAGATCTGTAGTCCCTACATCTCATAGTATGCGAGAAT 300
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QY 6320 GTGAAGCTCTTGTGACTAGGATGCAATCATGGTCAATGGAAGTTTCAGGTGCTTGGCA 6379
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Db 361 GTGTCCAGCATCTGAACAACACAGTGTGGAGATGGTTATACATAGTTGTACGAATAGC 420
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QY 6438 AGGTCCAAACCCGACCTGAAGCTGTCCAGGATTTCTTTGGACTTCGATTTCTCTGGAAG 6497
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Db 421 AGGTCCAAACCCGACCTGAAGCTGTCCAGGATTTCTTTGGACTTCGATTTCTCTGGAAG 480
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QY 6498 TGTTCT--AAAAGAAACACCGGAACATGCTACAAATACCAGCTTCATCTTTCATTAICT 6555
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Db 481 TGTCCTACACAGAGAAACATCGAAACATGCTTCAGTACCAGCTTCATCTCTCTGTCAT 540
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Db 541 TCTTAGCCAGGATTTACGATCCTCTCCAGAGCAAAAGCGACTCCACATAGAGAC 6600
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QY 6616 TACTCTGTCTCTCAGACACACTTGACCAAGTATTGT--GAACTTTGCACAGGACCAA 6673
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Db 601 TACTCTGTCTCTCAGACACACTTGACCAAGTACTCGTGAACCTTGTGCAAGGCCCAA 660
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QY 6674 GTGATGATGACCACTTA-AAAGACCTCTCATTACACAAACACGACACTAGTGGACGTT 6732
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Db 661 GTGATGATGACCACTTACGAGGACCTGTCTACTGCCCAACACCCGACAGAGCTGTGGAT 720
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QY 6733 G 6733
Db 721 G 721

RESULT 6
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LOCUS 602965918F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5116373 5',
DEFINITION mRNA sequence.
ACCESSION BI248317
VERSION BI248317.1 GI:14794093
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 720)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11283 row: d column: 06
High quality sequence start: 7
High quality sequence stop: 691.

FEATURES
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BASE COUNT 206 a 162 c 178 g 174 t

ORIGIN

Query Match 7.8%; Score 526.6; DB 13; Length 720;
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Matches 626; Conservative 0; Mismatches 69; Indels 8; Gaps 5;

QY 6056 AAGAAGTTGCCAAGTTGGTGGTGGCGGATTCGGAAA---CTGGGCTTCGTGAAGTATG 6112
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Db 6 AGGAAGTTGTCAGTTGGTGAAGGGGCAATCTGCAAACTGTGGCGTGAAGTATG 65
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QY 6113 GAGAAAATATGCTGTACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCATGG 6172
|||||
Db 66 GAGAAAATATGCTGTACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCATGG 125
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QY 6173 CTTTGTATCGCGGGCTTCCTGTGTGTCTGGATGAACCCACAGGATGGATGCCA 6232
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Dd	771 CCCCCTGCTCCTTGTGATGAACCCACCACAGGCAT-GATCCCAAAGCCGCGCATTC-- 715	
Qy	6250 TGGAAITGCGCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACATCTCATAGT 6309	
Dd	714 GTGAATTGCGCCTAAGTATCGTCAAGGAAGAAGATCAGTAGTGCTTACATCTCATAGT 655	
Qy	6310 ATGGAAGAATGTGAAGCTCTTTTGCTACTAGGATGGCAATCATGGTCAATGGAGGTTTCAGG 6369	
Dd	654 ATGGAAGAATGTGAAGCTCTTTTGACCCAGGATGGCAATATTGGTCAATGGAGGTTTCAGG 595	


```
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR0-UT0047-170
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                  profiles into the pUC 18 vector. Reverse transcription of
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                  low stringency conditions."
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Db      |||
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Db      |||
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RESULT 12
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DEFINITION BF076322.1 GI:10870075
ACCESSION  BF076322.1
VERSION     BF076322.1
KEYWORDS    EST.
SOURCE      cow.
ORGANISM   Bos taurus
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            Bovidae; Bovinae; Bos.
            1 (bases 1 to 554)
            Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W., Rohrer,G.A., Chitko-McKown,C.G.,
            pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keeler,J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
            21180013
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
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QY 1074 GATGAAGATTGGAGTCTAGTCTCTTCCGCAATATCTGGAAGACCTCTGAAGCCGCT 1133
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 QY 1253 AACTCAGCCCAAGATCTGACCTTCATGAGAGACAGCCAAAGATGGACCTTGTCCGGA 1312
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RESULT 13
 LOCUS
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 BP250020B10D9 Soares normalized bovine placenta Bos taurus cDNA
 clone BP250020B10D9 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

518 bp mRNA linear EST 10-OCT-2000
 BP250020B10D9 Soares normalized bovine placenta Bos taurus cDNA
 clone BP250020B10D9 5', mRNA sequence.
 BP042703
 BP042703
 BP042703.1 GI:10759758
 EST.
 Cow.
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 518)
 Lewin,H.A., Soares,M.B., Rebeiz,M., Fardinas,J., Liu,L. and Larson
 J.H.
 Bovine ESTs
 Unpublished (2000)
 Contact: Lewin, H. A.
 W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3203-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross_match from Washington University Genome Center PHRAP suite.
 This sequence is vector free and at least 200 bp in length.
 PCR Primers
 FORWARD: TAATGAGTCACTATAGG
 BACKWARD: ATTAACCTCACTAAG
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 1. 518
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 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6(9): 791-806."

FEATURES

source

BASE COUNT 122 a 121 c 153 g 122 t

Query Match 6.4%; Score 433.2; DB 12; Length 518;
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Db 1 GAGACCAACCCAGGCAATCCAGACCAATCTCTGTTTCATGAGTGTGCAACCTGAACAAG 60

QY 1528 CTAGAACCCATAGCAACAGAGTCTGGCTCATCAACAAGTCCATGAGTCTGATGAG 1587

Db 61 CTAGAACCCATAGCAACAGAGTCTGGCTCATCAACAAGTCCATGAGTCTGATGAG 120

QY 1588 AGGAAGTCTGGGCTGGTATTGTTCACTGGAATTACTCCAGGCAGCATTTGAGTGGCC 1647

Db 121 CGCAATCTGGGCTGGGCTGGTATTGTTCACTGGAATTACTCCAGGCAGCATTTGAGTGGCC 180

QY 1648 CATCATGTCAAGTACAGATCCGAATGGACATTTGACATTTGGAGAGGACAAATAAATC 1707

Db 181 CATCATGTCAAGTACAGATCCGAATGGACATTTGACATTTGGAGAGGACAAATAAATC 240

QY 1708 AAGGATGGTACTGGGACCCCTGGTCTCGAGCTGACCCCTTTGAGGACATCGGGTACGTC 1767

Db 241 AAGGATGGTACTGGGACCCCTGGTCTCGAGCTGACCCCTTTGAGGACATCGGGTACGTC 300

QY 1768 TGGGGGGGCTTGGCCCTACTTGCAGGATGTGGTGGAGCAGGCAATCATCAGGGTGTGACG 1827

Db 301 TGGGGGGGCTTGGCCCTACTTGCAGGATGTGGTGGAGCAGGCAATCATCAGGGTGTGACG 360

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Db 361 GGCACCGAGAGAAACATGGTGTCTATATGCAACAGATGCCCTATCCCTGTTAGCTGTAT 420

QY 1888 GACATCTTCTCGGGGTGATGAGCGGTCATGCCCCCTTCATGAGCGTCCCTGCGATT 1947

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RESULT 14
 BE715104

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

BE715104 463 bp mRNA linear EST 12-SEP-2000
 MR3-HT0737-060700-004-b09 HT0737 Homo sapiens cDNA, mRNA sequence.

BE715104

BE715104.1 GI:10103369

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 463)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MR3-HT0737-060
700-004-B09&t3=2000-07-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 461.

FEATURES

Location/Qualifiers
1..463
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0737"
/dev_stage="Adult"
/note="Organ: head neck; Vector: puc18; Site: SmaI;
Site: SmaI: A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles mRNA and cDNA amplification were performed under
low stringency conditions."
147 a 105 c 111 g 100 t

BASE COUNT
ORIGIN

Query Match 6.3%; Score 428.8; DB 12; Length 463;
Best Local Similarity 97.3%; Pred. No. 2.7e-106;
Matches 436; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 4480 GCAGATATCCTTCAGACCTGCAGGAGAAACATTCGGATTATCTGTTGAAGAGCTAT 4539
Db 6 GTAGATATCCTTCAGACCTGCAGGAGAAACATTCGGATTATCTGTTGAAGAGCTAT 65
QY 4540 GTCAGATATGACCAAGCTTAAAGACAGATCTGGTGAATGAGTTAGGTATGGC 4599
Db 66 GTCAGATATGACCAAGCTTAAAGACAGATCTGGTGAATGAGTTAGGTATGGC 125
QY 4600 GGTCTTCCCTGGGTGTCAGTATATCTCAAGCACTTCTCCGAGTCAAGAAGTTAATGAT 4659
Db 126 GGTCTTCCCTGGGTGTCAGTATATCTCAAGCACTTCTCCGAGTCAAGAAGTTAATGAT 185
QY 4660 GGCATCAACAATGAGAAACACCTTAAGCTGGCCAGAGACAGTTCTGCAGATCGATTT 4719
Db 186 GGCATCAACAATGAGAAACACCTTAAGCTGGCCAGAGACAGTTCTGCAGATCGATTTA 245
QY 4720 CTCACAGCTTGGAGATTATGACAGGACTGCACAGGACCAAGAAATATGTCAGAGTGTGG 4779
Db 246 CTCACAGCTTGGAGATTATGACAGGACTGCACAGGACCAAGAAATATGTCAGAGTGTGG 305
QY 4780 TTCAATAACAAGGCTGGCATGCAATCAGCTCTTCTGTAATCTCATCAACAATGCCATT 4839
Db 306 TTCAATAACAAGGCTGGCATGCAATCAGCTCTTCTGTAATCTCATCAACAATGCCATT 365
QY 4840 CTCGGGCCAACCTGCMAAAGGAGAGAACCCCTAGCCATTATGGAATTACTGCTTTCAAT 4899
Db 366 CTCGGGCCAACCTGCMAAAGGAGAGAACCCCTAGCCATTATGGAATTACTGCTTTCAAT 425
QY 4900 CATCCCTGGAATCTCACAAGCAGCAGC 4927
Db 426 CATCCCTGGAATCTCACAAGCAGCAGC 453

RESULT 15
BM153383
LOCUS
DEFINITION
BM153383 427 bp mRNA linear EST 30-NOV-2001
TCBAP2D11628 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens CDNA clone TCBAP1162, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BM153383
GI:17178477
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 427)
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr.,
Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
Pediatric Leukemia CDNA Sequencing Project (2001)
Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@tccc.org

Seq primer: M13 primer.

Location/Qualifiers

source

1..427

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="TCBAP1162"

/leukemia="Pediatric pre-B cell acute lymphoblastic

leukemia Baylor-HGSC project=TCBA"

/sex="male"

/tissue_type="leukopheresis"

/cell_type="pre-B cell"

/dev_stage="pediatric 2 years"

/lab_host="DH10B"

/note="vector: lambda pSB; Site:1: BamHI; Site:2: EcoRI;

First strand cDNA was primed with an anchored

XhoI-oligo(dT) primer [5'GGAGACTGAGCGCCGAGGAGAG(T)VN

3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand

was primed with a BamHI-dC primer

[5'AGAGAGTCGGATCGCGCGCAATATAAT(C) 3'].

Double-stranded cDNA was then digested with BamHI and XhoI

and directionally cloned into the BamHI and SalI sites of

lambda pSB vector. Library went through one round of

normalization. Library was constructed by Wei Yu at RIKEN

of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,

Itoh M, Nagaoka S, Sasaki N, Okazaki Y, Muramatsu M,

Schneider C, Hayashizaki Y, High efficiency selection of

full-length cDNA by improved biotinylated cap trapper.,

DNA Res 4: 1, 61-6, Feb 28, 1997")

BASE COUNT 85 a 104 c 126 g 112 t

ORIGIN

Query Match 6.3%; Score 425.4; DB 13; Length 427;

Best Local Similarity 99.8%; Pred. No. 2.2e-105;

Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1740 TGACCCCTTTGAGGACATCGGTACGCTCTGGGGGGCTTCGCCTACTTCGAGGATGGT 1799

Db 1 TGACCCCTTTGAGGACATCGGTACGCTCTGGGGGGCTTCGCCTACTTCGAGGATGGT 60

QY 1800 GGAGCAGGCAATCATCAGGCTGTGACGGCCACCGAGAGAAACTGGTCTATATGCA 1859

Db 61 GGAGCAGGCAATCATCAGGCTGTGACGGCCACCGAGAGAAACTGGTCTATATGCA 120

QY 1860 ACAGATGCCCTATCCCTGTTAGCTTGTATGACATCTTCTCGGGGTGATGAGCGGTCAAT 1919

Db 121 ACAGATGCCCTATCCCTGTTAGCTTGTATGACATCTTCTCGGGGTGATGAGCGGTCAAT 180

QY 1920 GCCCTCTTCATGACCTGGCTGGGATTTACTCAGTGGCTGTGATCATCAAGGCGATCGT 1979

Db 181 GCCCTCTTCATGACCTGGCTGGGATTTACTCAGTGGCTGTGATCATCAAGGCGATCGT 240

QY 1980 GTATGAGAGGAGGACGCGCTGAAAGAGACCATGCGGATCATGGGCTGCACAAACAGCAT 2039

Db 241 GTATGAGAGGAGGACGCGCTGAAAGAGACCATGCGGATCATGGGCTGCACAAACAGCAT 300

QY 2040 ACTCTGGTTAGCTGTTTCATTAGTAGCCTCATTCCTCTCTTGTGAGCGCTGGCCTGCT 2099

Db 301 CCTCTGGTTAGCTGTTTCATTAGTAGCCTCATTCCTCTCTTGTGAGCGCTGGCCTGCT 360

QY 2100 AGTGGTCATCCTGAAGTAGGAAACCTGCTGCCCTACAGTATCCCGAGCGTGTGTTTCT 2159

|||||
Db 361 AGTGGTCATCCTGAAGTAGGAAACCTGCTGCCCTACAGTGATCCAGCGTGTGTGTGT 420
QY 2160 CTTCCCTG 2166
|||||
Db 421 CTTCCCTG 427

Search completed: April 3, 2003, 16:38:07
Job time : 7723.53 secs